GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model April 4, 2001, 13:03:57; Search time 18 Seconds (without alignments) 670.578 Million cell updates/sec

Run on:

US-09-466-778-11 1857 1 MTGPGKHKCECKSHYVGDGL......ALAAXSYFRINRKTIGFXHF 353 Title: Perfect score: Sequence:

268485 seqs, 34193795 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_36:\* 1: /srnc1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES Description	Tumour necrosis	Tumour necrosis Tumour necrosis	Amino acid sequer	Rat proteoglycan	Human link pro	Chicken proteo	Human proteoglyca	Human proteogl	Neurocan core pro	Cloned duplicate	Rat brain-enrich
SUMMARIES	R26044	W13654 W84087	X13381	Y57083	Y57080	Y57082	Y57081	Y57084	R46627	W74523	R77034
DB	13	7 7 7 8	20	21	21	21	21	21	15	19	16
% Query Match Length DB	277	277	360	339	354	355	354	354	1257	252	355
% Query Match	14.1	14.1	10.1	9.1	8.9	8.9	8.8	8.8	8.5	8.4	8.4
Score	262	262 262	187.5	169.5	165.5	165.5	163.5	163.5	157.5	156.5	155.5
Result No.		73 F	4	2	φ	7	∞	6	10	11	12

>	Amino acid sequenc	Amino acid sequenc	Versican. Homo sa	Rat brevican core	Cat brain-enriched	Human cartilage li	Murine delta prote	Amino acid sequenc	Human signal pepti	Amino acid sequenc	×	Human nel-related	C-Delta-1 polypept	C-Delta-1 polypept	Chick delta protei	Metastasis-specifi	Human 5' EST secre	Haematopoietic CD4	Human haematopoiet		Human CD44 antigen	Epithelial CD44 An		Human CD44 antigen		ಹ	M-Delta-1 polypept	Truncated human de	Proliferation and	Proliferation and	Truncated human de	Proliferation and
R85442	W59882	W74522	R12609	R85443	R77035	R57350	X79028	Y13379	Y87287	W56249	R05222	W37500	W11719	W00876	¥79029	R14768	Y12323	R20816	R91444	W80453	W86200	R20817	R91445	W80454	W89151	R25079	W11720		W18348	834	W75495	35
16	9	19	12	16	16	15	21	20	21	19	11	18	18	18	21	12	20	13	17	19	20	13	17	19	20	13	18	20	18	18	20	18
912	528	116	2409	806	378	354	722	322	322	322	2189	810	727	740	728	503	116	361	361	361	361	493	493	493	493	1480	722	512	520	702	702	723
8.4	8.3	•	8.1	8.0	7.9								5.4			5.3						•	•			•		•				5.0
155.5	0	151		148	-	-	114.5	109	109	107	107	105	99.5	99.5	98.5	97.5	97	96	96	96	96	96	96	96	96	95.5	94.5	93.5	93.5	93.5	93.5	93.5
13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

R26044 standard; Protein; 277 AA 03-FEB-1993 (first entry) RESULT R26044

TNF; chronic inflammatory conditions; rheumatoid arthritis; sepsis; Tumour necrosis factor-induced glycoprotein TSG-6.

cancer; infections.

Homo sapiens

/\*tag= c /note= "potential N-glycosylation site" 258..260 /\*tag= d /note= "potential N-glcyosylation site" /note= "potential N-glycosylation site" 118..120 a "putative signal sequence" Location/Qualifiers /\*tag= b 1..19 /\*tag= /note= Peptide Region Region Region 

W09212175-A

23-JUL-1992

92WO-US00333. 14-JAN-1992;

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Vilcek J, Wisniewski H;
                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1999
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14-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis;
                               TSG-6 DNA
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSG-6; human; tumour necrosis factor-stimulated gene-6 protein; treat; inflammatory disease; cancer-related pathology; inhibit; metastasis; invasive tumour growth; rheumatoid arthritis; cachexia; atherosclerosis;
                                                                                                                                                                   The sequence is that of tumour necrosis factor (TNF) induced glycoprotein TSG-6. TSG-6 is induced in connective tissue by TNF and interleurin-7, and interferes with cell adhesion to ther cells or the extracellular matrix. It and antibodies specific for it are useful in diagnosis (including identifying susceptibility) and treatment of various disorders associated with cytokine (injactivation e.g. chronic inflammation (esp. where associated with proteoglycan breakdown, such as rheumatoid arthritis) cancer (esp. development of metastases) and infections (esp. those caused by Gram negative bacteria).
                                                                                                                                                                                                                                                                                                                                                       52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                    : ||:| : |:||||: :|: | | :||| || :| :|:||||: || 32 eraagvyhrearsgkykltyaeakavcefegghlatykqleaarkigfhvcaagwmakgr 91
                                                                                             Tumour necrosis factor-induced (glyco)protein mol. TSG-6 and its antibody - for treatment and diagnosis of chronic inflammatory conditions e.g. rheumatoid arthritis, infections, sepsis and
                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                             14.1%; Score 262; DB 13; Length 277; 43.3%; Pred. No. 1.6e-19; Live 16; Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                             112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systemic lupus erythematosus; rational drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor-stimulated gene-6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vilcek J, Wisniewski H;
                                         Wisniewski HG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W13654 standard; protein; 277 AA
                                                                                                                                                 Claim 1; Fig 3; 122pp; English
 91US-0642312
                     (UYNY ) UNIV NEW YORK STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-132619/12.
                                                              WPI; 1992-284330/34
                                          Vilcek J,
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                               277 AA;
                                                                          N-PSDB; Q27190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSG-6; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cronstein BN,
14-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9704075-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                               Query Match
                                          Lee TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W13654;
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W13654
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This protein is the human tumour necrosis factor-stimulated gene-6 protein (TSG-6). It can be used in a claimed pharmaceutical composition for treating inflammatory diseases and disorders, or cancer-related pathologies. The composition or DNA encoding TSG-6 may be used to inhibit tumour metastases, invasive tumour growth or cancer-related pathologies. They may also be used in the treatment of inflammatory conditions including rheumatoid arthritis, systemic lupus erythematosus, and infections such as cachexia, artherosclerosis etc. TSG-6 can also be used to design drugs to treat these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; cytokine; immune disorder; autoimmune disorder; infection; inflammatory disease; neurodegenerative disease; cancer; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor stimulated gene 6; TSG-6; recombinant; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||:| : |:||||: || :||| :||| :|||||: || 32 eraagvyhrearsgkykltyaeakavcefegghlatykqleaarkigfhvcaagwmakgr 91
New TSG-6 compositions to treat inflammatory diseases and cancer can be complexed with inter-alpha-inhibitor, to treat auto-immune disease, cancer-related pathology etc. can also be administered as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "potential Asn-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 262; DB 18;
; Pred. No. 1.6e-19;
16; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "mature protein"
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                                                                                                                                                                          Claim 2; Page 58-59; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W84087 standard; Protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0242097.
91US-0642312.
93US-0024868.
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118..120
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258..260
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                                                                                                                                                    protein. A proxaryotic host cell transformed, or a entaryotic host cell transformed, or a entaryotic host cell transformed, or a entaryotic host cell transferced with expression vectors containing the TSG-6 nucleic acid are used to produce recombinant human TSG-6 protein. TSG proteins, peptide fragments of TSG proteins or antibodies to TSG proteins are useful for diagnosis or therapy of diseases mediated by cytokine activity or inactivity, such as immune and autoimmune disorders, infections, inflammatory diseases, neurodegenerative diseases, cancer and alcohol-
                                                                                                                                        represents a human tumour necrosis factor stimulated gene 6 (TSG-6)
                                                                                                                                                                                                                                                                                                                                                                                                             52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis; 2011inger Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; Alz, neuropathy; elibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding tumour necrosis factor stimulated gene 6 protein - useful for producing recombinant protein for diagnosis and therapy of disease e.g. immune disorders or cancer
                                                                                                                                                                                                                                                                                                                                              14.1%; Score 262; DB 20; Length 277; 43.3%; Pred. No. 1.6e-19;
                                                                                                                                                                                                                                                                                                                                                                               43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of protein PRO271.
                                                                                                        Claim 2; Fig 3A-C; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y13381 standard; Protein; 360 AA
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970S-0059115.
970S-0059117.
970S-0059119.
970S-0059121.
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97US-0059184.
97US-0059263.
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970S-0062125.
970S-0062285.
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                                                                                                                                                                                                                                                                                                                                                                               45; Conservative
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WPI; 1999-059056/05
                                                                                                                                                                                                                                                                 induced hepatitis.
                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                 277 AA;
                  N-PSDB; V71778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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17-SEP-1997;
17-SEP-1997;
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15-OCT-1997;
17-OCT-1997;
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                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                Query Match
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The CDNA sequences are obtained transmentate numen process.

The CDNA sequences are obtained from CDNA libraries, propared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The cDNA sequences are obtained brain, fetal liver and fetal retina. The conceptions of propertides have specific uses based on their homology to known polypeptides, e.g. PRO21 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosa lessions (e.g. enterocolitis, Zollinger Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abbornal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth cancer survival of nerve cells including Parkinson's diseases, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a antiet-thrombotic agent; PRO287 polypeptides and portions may have chromotic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endomentium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
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not involved in autoimmunity. These peptides and proteins are used in the method of the invention which involves administering an NTTA as an autoimmune response associated with an autoimmune disease. The autoimmune response associated with an autoimmune diseases such as immunotherapeutic agent, to a host afflicted with an autoimmune diseases. The immunotherapeutic agent is used to treat autoimmune diseases such as immunotherapeutic agent is used to treat autoimmune diseases such as immunotherapeutic agent is used to treat autoimmune diseases. The immune responses. The NTTA induces regulatory tolerance by elicitation of participating in the immune response. The NTTA are capable of reconition by substantial populations of uncommitted T cells which can be primed, or biased, towards regulatory responses to provide effective treatment. The immune responses are responses even when target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory T cell response. NTTAs as agents
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                                                                                         10.1%; Score 187.5; DB 3
30.8%; Pred. No. 1.8e-11;
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promoting tolerance are anticipated to be safer than use of target
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                                                                                                         9.1%; Score 169.5; DB 2.30.8%; Pred. No. 1.3e-09; tive 20; Mismatches 52
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NTTA are effective in regulating undesirable immune responses even rarget determinants used as agents promoting tolerance agents have to induce an effective regulatory T cell response. NTTAs as agents promoting tolerance are anticipated to be safer than use of target
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Pred. No. 3.8e-09;
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                                                                                                                                                                                                      Length 355;
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                                                                                                                                                                                                  Score 165.5; DB 21;
Pred. No. 3.8e-09;
                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    124 G--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                       Y57081 standard; protein; 354 AA.
                                                                                                                                                                                                                                    26;
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                                                                                                                                                                                                                                                                                                   136 grykce----viegl----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-052905/04.
                                                                                                                                                                                                                  Similarity
                                                                                                                                                     AA;
                                                                                                                                                     352
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                                                                                                  promoting to
determinants
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Best Local
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thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory immune responses. The NTTA induces regulatory tolerance by elicitation of regulatory T cells among T cells recognizing the NTTA but not participating in the immune response. The NTTA are capable of recognition by substantial populations of uncommitted T cells which can be primed, or biased, towards regulatory responses to provide effective treatment. The NTTA are effective in regulating undesirable immune responses even when target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory T cell response. NTTAs as agents promoting tolerance are anticipated to be safer than use of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neglected target tissue antigen; NTTA; autoimmunity; autoimmune response; immunotherapeutic agent; insulin dependent diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis; uvecretinitis; inflammatory response.
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                                                                                                                                                                                                                                                                                                                                             GQYKLIFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                            227
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                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                         Length 354;
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                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                         8.8%; Score 163.5; DB 2:
30.1%; Pred. No. 6.1e-09;
iive 21; Mismatches 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human proteoglycan link protein precursor #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | |: :|| : :|| 228 ggntvpgvrnygfwdkdksrydvfcf 253
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autoimmune response associated with an autoimmune disease. The immunotherapeutic agent is used to treat autoimmune diseases such as insulin dependent diabetes mellitus, multiple sclerosis, autoimmune thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory immune responses. The NTTA induces regulatory tolerance by elicitation of regulatory T cells among T cells recognizing the NTTA but not by substantial populations of uncommitted T cells which can be primed, or biased, towards regulatory responses to provide effective treatment. The NTTA are effective in regulating undesirable immune responses even when target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory T cell response. NTTAs as agents parametrizative and a sagents promoting tolerance agents have failed the induce an effective regulatory T cell response. NTTAs as agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurocan; cell adhesion; leukocyte-endothelial cell recognition; lipid; tissue-related inflammation allergy; cellular; humoural; carbohydrate; hypersensitivity; trauma; neuronal development; cell transport; enzyme; infection; diagnosis; lectin; versican; aggrecan; gelsolin; saccharide; receptor; cell recognition; membrane cytoplasmic protein; nucleoside.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                    Gaps
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431
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30.1%; Pred. No. 6.1e-09;
iive 21; Mismatches 52
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gqntvpgvrnygfwdkdksrydvfcf 253
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Modified-site

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Eukaryotic neurocan polypeptide(s) with epidermal growth factor, lectin or complement binding activity – used in the diagnosis,
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/note= "Used for primer design"
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                "O-linked glycosylation
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/note= "Used in primer design"
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                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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This sequence represents a neurocan polypeptide. This protein has several biological activities, including cell adhesion, leukocytenendothelial cell recognition, tissue-related inflammation allergies, endothelial cell recognition, tissue-related inflammation allergies, cellular and/or humoural hypersensitivity, trauma, neuronal development, and cell transport and/or infection. Compositions containing them can be used as modulators of these conditions, and may be used as therapeutic, diagnostic, and/or research tools.

Neurocan peptides can be used to mimic proteins, such as lectins, cell adhesion molecules, versicans, agreeced or gleolins, as receptor or effector subtypes. The protein can be used to treat diseases involving a qualitative or quantitative pathological abnormality of cell adhesion or leukocyte-endothelial cell recognition, or a functionally associated molecule such as a membrane cytoplasmic protein, lipid, carbohydrate, saccharide, nucleoside, enzyme or ion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 LETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVG 163
                                                                                                                                                                                                                                                                                                                                                                                               47 DLHFQDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGW 106
                                                                                                                                                                                                                                                                                                                                                                                                                          150 dlvtlevtgvvfhyraardryaltfaeageachlssatiaaprhlgaafedgfdncdagw 209
                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
treatment or research of hypersensitivity and allergic diseases
                                                                                                                                                                                                                                                                                                                                    DB 15; Length 1257;
                                                                                                                                                                                                                                                                                                                                                                  53; Indels
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                                                                                                                                                                                                                                                                                                                                 8.5%; Score 157.5; DB 34.2%; Pred. No. 1.8e-07 tive 19; Mismatches 5
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                              Claim 1; Page 69-75; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W74523 standard; Protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97EP-0102951.
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                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 34.2.
Loca 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= '
240
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SCHMIDT G.
UHLENKUEKEN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 133
                                                                                                                                                                                                                                                                                        1257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP861903-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1998
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W74523
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354..648
                                                                WPI; 1995-366390/47
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                           (UYYA ) UNIV YALE
                                                                          T01475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                            Hockfield S,
        08-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1996
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                                                                                                                                                                                                                                                  Sequence
                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R85442;
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                                                                                                                                                                                                                                                                                                                                                                          256
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                                                                                                                                                                                                                                                                                       150 strytldfdragraclgnsailatpeglgaayedgfhqcdagwladgtvrypihtpregc 209
                                                                                                                                                                                                                                        57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                             117 AFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCY--RMKDVNCTXKVGYVGDGFSYSGN 171
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                  172 LLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEH------LTDLSIRGTLFXPQNSG
                                                                                                   This is the amino acid sequence of the cloned duplicate of human aggrecan G1-B domain, starting from the RBS of the tet o/p of pr HA-20, used in the method of the invention which involves the production of homogeneous polysaccharides from heterogeneous polysaccharides. The oligonucleotides and polysaccharides are useful for the diagnosis and therapy of diseases.
                                                                                                                                                                                                                      15;
                                                                                                                                                                                                  Length 252;
                                   Production of homogeneous polysaccharides from heterogeneous polysaccharides used for diagnosis and therapy of diseases comprises immobilisation on support e.g. polymer matrix and selective cleavage with e.g. glucosidase or hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -enriched hyaluronan binding protein; BEHAB; glioma;
tumour; hyaluronic acid; proteoglycan; tumour marker;
                                                                                                                                                                                                8.4%; Score 156.5; DB 19; Length 25.9%; Pred. No. 2e-08; tive 29; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat brain-enriched hyaluronan binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig_fold_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
23..157
/label= Ig_fold_doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        R77034 standard; Protein; 355 AA.
                                                                                  Example 1; Fig 4; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158..257
/label= PTR1
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/label- PTR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                 Query Match
Best Local Similarity 25.95
Matches 49; Conservative
                   N-PSDB; V53720; V53721.
        WPI; 1998-449114/39
                                                                                                                                                                                                                                                                                                                                                       223 LGENETLSG 231
                                                                                                                                                                                                                                                                                                                                                                          210 ygdkdefpg 218
                                                                                                                                                                       252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brain-enriched
brain tumour; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09527785-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic.
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                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                           R77034;
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R77034
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Novel rat brain-enriched hyaluronan binding (BEHAB) protein (R77034) is isolated from brain tissue and has a high degree of homology to members of the proteoglycan tandem repeat family of hyaluronan binding proteins. It includes 2 domains, PTR1 and PTR2, thought to be involved in hyaluronan binding. BEHAB is expressed at markedly increased levels in glioma tissue, and can therefore be used as a diagnostic marker. Recombinant BEHAB is obtd. by expression of the isolated encoding cDNA sequence (T01475) in procaryotic or eucaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 qcdagwlsdqtvrypiqnpreacygdmdgypgvrnygvvgpddlydvycyae---dln- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 QDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETG 110
                                                                                                                                                                                                                                             Mammalian brain-enriched hyaluronan-binding protein and its {\tt DNA} -useful as diagnostic marker for detection of brain tumours and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- NGQCHADAKCVDLHF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brevican; chrondroitin sulphate proteoglycan; glial cell; axon; neurofibromatosis; gliosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 RVAYPTAFASQNCGSGVVGIVDYGPRPN-----KSEMWDVFCYR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Protein-like_tandem_repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Immunoglobulin-like_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 155.5; DB 1.
27.9%; Pred. No. 4.3e-08;
live 21; Mismatches 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ECKSHYVGDGLNCEPEQLPIDRCLQD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R85442 standard; Protein; 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine brevican core protein.
94US-0225477
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Щ
                                                                                                                                                                                                                                                                                                         neuro:pathological states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.99
Matches 46; Conservative
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                                                                                                                Jaworski
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Feng P,
Su JY;
                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                         s;
                                                                                                                                                                                                                                                                                                                                                                                                    57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                               Mammalian brevican protein - directs/inhibits axonal growth, used in treatment of neuro-fibromatosis and in detection of gliosis
                                                                                                                                                                                                                                                                                                                                                        10 ECKSHYVGDGLNCEPEQLPIDRC-----LQDNGQCHADAKCVDLH----FQDTTVG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEF (HSXCK41); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                       2 Overlapping cDNA clones obtd. from a bovine brain cDNA library were combined (see T05627) to provide cDNA coding for bovine brevican (R8542). The brevican can be used to modulate axonal growth and to raise antibodies used in detection of gliosis.
                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                        DB 16; Length 912;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the cDNA clone BEF (HSXCK41).
                                                                                                                                                                        Yamaguchi Y;
                                                                                                                                                                                                                                                                                                                                        :99
                                                                                                                                                                                                                                                                                                                                                                                                                         117 AFASQNCGSGVVGI-----VDYGPRPNKSEMWDVFCYR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                  316 vtpsqrcggglpgvktlflfpnqtgfpnkhsrfnvycfr 354
                                                                                                                                                                                                                                                                                                                        8.4%; Score 155.5; DB 28.3%; Pred. No. 1.8e-07
                                           685.814
/label= Lectin-like_region
815.875
                                                                                                                                                                                                                                                                                                                                       23; Mismatches
                             649..684
/label= EGF-like_repeat
                                                              815..875
/label- CRP-like_region
                       /label= Central_region
                                                                                                                                                                       Yamada H,
                                                                                                                                                                                                                                        Claim 2; Page 42-44; 73pp; English.
                                                                                                                                                       (LJOL-) LA JOLLA CANCER RES FOUND.
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                                                                                                                       95WO-US03747.
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                        Watanabe
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                        WPI; 1995-351200/45.
                                                                                                                                                                                                                                                                                                912 AA;
                                                                                                                                                                                                N-PSDB; T05627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-1998;
                                                                                      WO9526201-A1
                                                                                                                       27-MAR-1995;
                                                                                                                                       28-MAR-1994;
                                                                                                                                                                        Shimonaka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-1998.
                                                                                                      05-0CT-1995
                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                Sequence
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•
                               Region
                                               Region
                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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This is the amino acid sequence of the cDNA clone BEF (HSXCK41), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NGOC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 HADAKCVDLHFQDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKY 99
                                                                                                                                                                                                                                                                              New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 HLCSAGWLETGRVAYPTAFASQNCGSGVVGI-----VDYGPRPNKSEMWDVFCYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; aggrecan G1-B domain; homogeneous polysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of the human aggrecan G1-B domain.
                                                                                                                                            Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 155; DB 19;
Pred. No. 8.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GKHKCECKSHYVGDGLNC----EPEQLPIDRCLQD-
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/note= "encoded by AAC"
                                                                                                                                         Σ̈
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 10A-10F; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                         Krissansen GW,
                                                               (AUCK-) AUCKLAND UNISERVICES LTD. (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%;
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97US-0034205
97US-0034204
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                            WPI; 1998-414099/35.
                                                                                                                                       Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 AA;
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                                                                                                                                                                                                                                  N-PSDB; V41923
21-JAN-1997;
21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                      or tumours
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7;

97EP-0102951.

22-FEB-1997;

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                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the human aggrecan G1-B domain, used in the method of the invention which involves the production of homogeneous polysaccharides from heterogeneous polysaccharides. The oligonucleotides and polysaccharides are useful for the diagnosis and therapy of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                      Production of homogeneous polysaccharides from heterogeneous polysaccharides used for diagnosis and therappy of diseases comprises immobilisation on support e.g. polymer matrix and selective cleavage with e.g. glucosidase or hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.1%; Score 151; DB 19; Length 116;
Best Local Similarity 35.8%; Pred. No. 2.4e-08;
Matches 34; Conservative 15; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AFASONC---GSGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | |: || |: :| :||:||: 74 htpregcygdkdefpgvrtygir-dtnetydvycf 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 4, 2001, 13:05:01 Job time: 64 sec
                                                                                                                                                                                                                                                                             Example 1; Fig 3; 19pp; English.
                               (LANS/) LANSING M.
(SCHM/) SCHMIDT G.
(UHLE/) UHLENKUEKEN J.
                                                                                                                                 WPI; 1998-449114/39.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 116 AA;
                                                                                                                                                     N-PSDB; V53715.
                                                                                                     Lansing M;
Db
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us-09-466-778-11.rspt

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April 4, 2001, 13:04:01; Search time 27.49 Seconds (without alignments) 1505.071 Million cell updates/sec
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1857
1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                             374700
GenCore version 4.5
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		,	Description	O9nrv3	Q9uf98 homo	093072 hошо	0				014594	088564		011610	17 002817 oryctolagus	077612	077611	011609	Q9ttb3	046380	Q9w6s4	Point out Parison
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			Score	1757	1468	662	645.5	264	177	169.5	162	161.5	161.5	160.5	153	153	151.5	151.5	126.5	120.5	110	109
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Q995y7 homo sapien Q33791 caenorhabdi Q23587 caenorhabdi Q23587 caenorhabdi P87357 brachydanio Q91bg4 xenopus lae O70474 rattus norv Q91tm2 homo sapien Q90556 gallus gall O57462 brachydanio O60494 homo sapien Q904X8 mus musculu Q904X8 mus musculu Q20204 caenorhabdi Q904X9 mus musculu Q20204 caenorhabdi Q904X9 mus musculu Q904X8 mus musculu Q904X9 musculus Q047F9 drosophila Q907F9 caratotheri Q91902 xenopus lae Q24530 vitis vinif P79754 fugu rubrip	S.  AA.  ie update)  ion update)  ion update)  ion update)  ion update)  ion update)  ithminidae; Buteleostomi;  ithminidae; Homo.  of human FELL sharing homology  ion atabases.  ion bb 4; Length 897;  bb 4; Length 897;	331; Conservative 3; Mismatches 19; Indels 0; Gaps 0; MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
4 09Y5Y7 5 093791 13 093791 13 091864 11 070474 11 070474 4 09NTM2 4 09NTM2 13 090556 13 057462 14 0907X8 5 020204 1 0904Y8 1 092491 5 020204 1 092491 5 020204 1 0947F9 1 000779 5 09V7F9 5 09V7F9 6 097569 1 070509 1 070509		3; Mismatches CEPEQLPIDRCLODNG
5.79 5.79	INARY Lrel. Lrel. Trel.; Cho; ; Prii, Cho; ;	Conservative KCECKSHYVGDGLM                   KCECKSHYVGDGLM KKLTFDKAREACANE
20 21 109 22 23 24 100 25 26 27 27 28 29 29 31 31 31 32 33 34 35 36 37 38 39 39 39 39 39 39 39 39 39 39	NRY3  ODNRY3  ODNRY3  OLOCT-2000 (TrEMBLr 01-0CT-2000 (TREMBLR 01-0CT-20	Matches 331; Conser 1 MTGPGKHKCECKS 
	RESULT QUARY 3 QUARY 3 DT DD DT DD DT DD DD DD DD DD DD DD DD	Mat Qy Db Qy Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
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300
                    817 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKG------SAGLFQQLSSRP 860
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  241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI
                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                   301 SRXLKAPPAPVTLXHTXLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALI33021; CAB61358.1; -.
INTERPRO; PR000538; -.
INTERPRO; IPR000551; -.
INTERPRO; IPR000561; -.
INTERPRO; IPR000561; -.
INTERPRO; IPR000561; -.
INTERPRO; IPR000561; -.
                                                                                                          29; Indels
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SEQUENCE 1069 AA; 115666 MW; 04B0960932164D63 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                           090F98;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHERICAL 115.7 KDA PROTEIN (FRAGMENT).
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80.5%; Pred. No. 1.2e-133;
                                                                                                                                                                                                                                     1069 AA
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PFAM; PF00193; X1ink; 1.
PRINTS; PR00191; EGFLAMININ.
PRINTS; PR01265; LINKMODULE.
PROSITE; PS01022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                           JECULENCE FROM N.A.

TISSUE-BONE MARROW;

MIDLINE-27191544, PubMed=9039502;

Magase T., Seki N., Inshikawa K., Ohira M., Kawarabayasi Y., Ohara C.

Tanaka A., Kotani H., Miyajima N., Nomura N.;

Frediction of the coding sequences of unidentified human genes. VI

The coding sequences of 80 new genes (ENAMO201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";

BNBL, D87433; BAA13377.1; -.

HSSP: P98066; ITSG.
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                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.6%; Score 662; DB 4; Length 22 40.2%; Pred. No. 4.9e-55; tive 47; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
237451 MW; 4A95460504129134 CRC64;
                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
MYELOBLAST KIAA0246 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR01265; LINKMODULE.
PS00022; EGF_1; UNKNOWN_5.
PS00086; CYTOCHROME_P450; UNKNOWN_2.
     2212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01186; EGF_2; 13.
PS01241; LINK; UNKNOWN_1.
PS01248; LAMININ_TYPE_EGF;
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.6'
Best Local Similarity 40.2'
Matches 143; Conservative
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR002049; -. PFAM; PF00008; EGF; 13. PFAM; PF00193; Xlink; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPROOD538; -. INTERPRO; IPROOD561; -. INTERPRO; IPROOD782; -. INTERPRO; IPROOL128; -.
                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 2212
                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Q93072
Q93072;
                                                                                                                                                        KIAA0246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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Fulop C., Kamath R.V., Li Y., Otto J.M., Salustri A., Olsen B.R., Glant T.T., Hascall V.C.;
Coding sequence, exon-intron structure and chromosomal localization of murine Thr.stimulated gene 6 that is specifically expressed by expanding cumulus cell-oocyte complexes.";
Gene 202:95-102(1997).
EMBL: 0830045; 1765.
MGD: MGI:1195266; Tnfip6.
INTERPRO; IPR000538; -.
INTERPRO; IPR000538; -.
INTERPRO; IPR000539; -.
PFPAM; PF0013; Xlink; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 DTTVGVFHLRSPLGQYKLJFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinàe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96262324; PubMed=8965652;
Li H., Domowicz M., Hennig A., Schwartz N.B.;
"Sl03L reactive chondroitin sulfate proteoglycan (aggrecan) mRNA
expressed in developing chick brain and cartilage is encoded by single gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Indels
                                                                                                                                                                                                                                                                                                                                                                                              1CD247228260B8F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) CHONROLITIN SULFATE PROTEOGLYCAN CORE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 264; DB 11;
43.3%; Pred. No. 1.2e-17;
tive 16; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brain Res. Mol. Brain Res. 36:309-321(1996).
EMBL; U78555; AAC60053.1; -.
HSSP; P08709; 1BF9.
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PROSITE; PS00010, ASX_HVROXYL; UNKNOWN_1.
PROSITE; PS000012; EGF_1; UNKNOWN_1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, Created)
  MEDLINE=98087423; PubMed=9427551;
                                                                                                                                                                                                                                                                                                                                                                                              30924 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO00152; INTERPRO; IPRO00152; INTERPRO; IPRO00561; INTERPRO; IPRO00561; INTERPRO; IPRO01742; INTERPRO; IPRO01304; INTERPRO; IPRO01304; INTERPRO; IPRO01304; INTERPRO; IPRO01306; PFAM; PPO00047; IG; I.PFAM; PPO0059; Iectin_c; IIPTAM; PPO0059; IIPTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.38
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                    PROSITE; PS01180; CUB; 1.
PROSITE; PS01241; LINK; 1.
PRODOM; PD000918; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00084; sushi; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFS-YSGNLLQVLMSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THVISRXLKAPPAPVTLX-----HTXLGXGIFXXIILVTGAV--ALAAYSYFRINRKTIG 349
                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.8%; Score 645.5; DB 4; Length 2570;
39.3%; Pred. No. 2.4e-53;
iive 48; Mismatches 154; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TGPGKHKCECKSHYVGDGLNC-EPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 (HYALURONATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 PSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGLGENETLSGRDIEHHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 NVSMFFYNDLVNGTTLQTRLGSKLLITDR---QDPLHPTETRCVDGRDTLEWDICASNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2393 NATLLSAN-ASQGKLLPAHSGLSLIISDAGPDNSSWAPVAPGTVVVSRIIVWDIMAFNGI
                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Wakaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                  Politz O., Guillot P., Gratchev A., Schledzewski K., Birk R., Hakiy N., Tebbe B., Orfanos C.E., Goerdt S.;
"Stablin-1: an endothelial-macrophage member of the fasciclin containing protein family associated with anglogenesis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ275213; CAB61827.1; -.
SEQUENCE 2570 AA: 275346 MW; 3123FABD7C8E2BF8 CRC64;
                                                                                                           Last sequence update)
Last annotation update)
                                             2570 AA
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                                                                                          Created)
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01-JUL-1997 (TrEMBLrel. 04, Last seq
01-OCT-2000 (TrEMBLrel. 15, Last ann
                                                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, STABILIN-1.
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TNFIP6 OR TNFAIP6 OR TSG6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 142; Conservative
                                             PRELIMINARY;
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                                        Q9NY15
                                                                Q9NY15
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RESULT
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PRODOM; PD000918; -; 2.
                                                                                                                                                                                                                                                    Created)
                                                                                                             125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                               229 GQNTVPGVRNYGFWDKDKSRYDVFCF 254
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10,
15,
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01-MAY-1999 (TrEMBLrel. 1C
01-OCT-2000 (TrEMBLrel. 15
NEUROCAN (PGCN-HUMAN).
CSPG3 OR NEUR.
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Matches 48; Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO00152; -.
INTERPRO; IPRO00436; -.
INTERPRO; IPRO00538; -.
 136 GRYKCE----VIEGL-
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                   57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                                                                                  426 TSVTVETASPREENVTREEITGIWAVPEEVTTSVSGTAF---TTGMAEVSSVEEAIAVTA 482
                                                                                                                                                                                                                    194 OCDAGWLADOTVRYPIHLPRERCYGDKDEFPGVRTYGVRETDETYDVYCYAEQMQGK--- 250
                                                                                                                                                                                                                                                                    117 AFASQNCGSGVVGI--VDYGPR----PNKSEMWDVFCYRMKDVNC-----TXKVG-YV 162
                                                                                                                                                                                                                                                                                                                                                                             --- SYSGNLLQVLMSFPSLTNFL 186
                                                                                                                                                            Gaps
                                                                                                                                                                                      10 ECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHA-------DAKCVDLHFQDTTVG
                                                                                                                                                                                                                                                                                                                                                                                                          368 GSAFTIQTVTQTEVELPLPRNVTEEEARGSIATLEPMEITSTATELYEAFTVLPDL--FA
                                                                                                                                                                                                                                                                                                                                                                                                                                        187 TEVLAYSNSSARGRAFLEHLTDL-----SIRGTLFXPQNSGLGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
Cyto J.M., CS-Szabo G., Kamath R.V., Liu W., Li Y., Glant T.T.;
"Molecular analysis of the murine link protein gene: 5' flanking, coding and 3' flanking sequence analysis; exon-intron structure; tissue distribution; and generation of transgenic mice."; EMBL; Submitted (OCT-1988) to the EMBL/GenBank/DDBJ databases.
EMBL; AF098460; AAD12253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                         98;
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                                                                                                                           Length 2109;
                                                                                                                        9.5%; Score 177; DB 13; Length 2 23.8%; Pred. No. 5.2e-08; tive 30; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 9.1%; Score 169.5; DB 11; Length Best Local Similarity 30.8%; Pred. No. 2.6e-08; Matches 45; Conservative 20; Mismatches 52; Indels
                                                                            38492D317D245A97 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 AA.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01241; LINK; 4.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PRODOM; PD000918; -; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                           223480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PS01241; LINK; 2.
PD000918; -; 2.
E 355 AA; 40340 MW;
                                                            Glycoprotein; EGF-like domain.
SEQUENCE 2109 AA; 223480 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 TPGLESASPFTIEDHLVQVT 502
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                                                                                                                          Query Match 9.55
Best Local Similarity 23.8
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; 1g; 1.
PFAM; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR00538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                             GDGF ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; |
PRODOM; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0921X7
                                                                                                                                                                                                                                                                                                                                              308
                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q921X7
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------EVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-990 FROM N.A.
Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Christensen M., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Christensen M., Gordon L., Kyle A., Quan G., Montgomery M., Ow D.,
Kobayashi A., Olsen A.O., Carrano A.V.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Ac003110; AAC80576.1;
EMBL; AC003110; AAB86655.1;
HSSP: P00740; IEDM.
                                                                                                                                                                                                                                                                                      Lennon G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1321;
                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; EGF-like domain.
SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;
                                                                                                                                                                                                                                                              MEDLINE-99013874; PubMed-9795216;
Prange C. K., Pennacchio L.A., Lieuallen K., Fan W.,
"Characterization of the human neurocan gene, CSPG3.
Gene 221:199-205(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 162; DB 4;
27.9%; Pred. No. 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 FXPQNSG--LG-----ENETL----SGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVG-VFHLRSP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                           311 ARAQCGGGLGVRTLYRFENQTCFPLPDSRFDAYCFKRPDLCKTNPCLNGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PRODOSO; BGFBLOOD.
PROSITE; PROMO201; BGFBLOOD.
PROSITE; PROMO10; BAX HYDROXIL; UNKNOWN_1.
PROSITE; PROMO12; C_TVPE_LECTIN_1.
PROSITE; PRO1187; EGF_2; 1.
PROSITE; PRO1187; EGF_2; 1.
PROSITE; PRO1187; EGF_2; 1.
PROSITE; PRO1187; EGF_2; 1.
PROSITE; PRO1187; EGF_1, EGF_1, EGF_2; 1.
PROSITE; PROFILE; EGF_1, EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) NEUROCAN CORE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                        363 ------CYPTETSYVCTCAPGYSGDOCELDFDECHSN 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 161.5; DB 1
29.1%; Pred. No. 8.6e-07;
tive 21; Mismatches 51
                                                                                                                                                                                                                                                         263 LLITDRODPLHPTET----RCVDG----RDTLEWDICASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GSGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 YGDRNSLPGVRSYGOR-EPGELYDVYCY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO00538; -
INTERPRO; IPR000561; -
INTERPRO; IPR000742; -
INTERPRO; IPR001304; -
INTERPRO; IPR001304; -
INTERPRO; IPR001881; -
INTERPRO; IPR00189; INTERPRO; INTERPRO; INTERPROS; IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9W6E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
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                                                                          57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AFASQNCGS---GVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYV-GDGFSYSGNL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 RAPREGCYGDMMGKEGVRTYGFR-SPQETYDVYCY-----VDHLDGDVFH---- 254
                                   55 VGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 161.5; DB 11; Length 655; 26.1%; Pred. No. 3.5e-07; ive 30; Mismatches 98; Indels 79;
                                                                                                                                                                                                                          PTAFASQNC --- GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-WISTAR KYOTO;
Lemire J.M., Braun K.R., Maurel P., Margolis R.U., Schwartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Wersican isoforms in vascular smooth muscle cells.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
R EMBL; APO72892; AAC26116.1; -..
R HYSEP; PO17292; HEGF.
R INTERPRO; IPRO00152; -..
R INTERPRO; IPRO00436; -..
R INTERPRO; IPRO00538; -..
R INTERPRO; IPRO01304; -..
R INTERPRO; IPRO01306; -..
R INTERPRO; IPRO01306; -..
R PFAM; PFO0008; EGF; 2..
R PFAM; PFO0009; AN 110; 2..
R PFAM; PFO0004; anshi; 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSICAN V3 ISOFORM.
602F2F37E4F1ECC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
VERSICAN V3 ISOFORM PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRODOIO; EGRBLOOD.
PROSITE; PRODOIO; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PRODO10; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PROBOIS; EGF_1; UNKNOWN_2.
PROSITE; PRO1186; EGF_2; 1.
PROSITE; PRO1187; EGF_CA; 1.
PROSITE; PRO1187; EGF_CA; 1.
PROSITE; PRO1187; CTYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74474 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                088564;
                                                                                                                                                                                                                                                                                                                                                                                                                                             088564
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33; Gaps

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226 NETLSGR-DIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRD 284
                                                                                                                                                                                                                                                                                                                                                                                                                    192 AA; 21606 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 8.2%;
Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     TISSUE=CARTILAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
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SEQUENCE
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Best Local S.
Matches 34
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002817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 NKFTFEEAGEECKTQD----ARLATVGELQAAWRNGFDRCDYGWLLDASVRHPVTVARAQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 WLETGRVAYPTAFASONCGS---GVVGIVDYGPRPNKSEMWDVFCY------- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSGNLLQV - - LMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGLGE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGLLGVRTLYRFENQTGFPT----, PDSRFDAYCFKRRMSDFSVSG---HPIDSESKE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDT --- TVG -- VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Versican V2 is a major extracellular matrix component of the mature bovine brain.";
J. Biol. Chem. 273:15758-15764(1998).
EMBL. AF060457; AAC24359.1; -.
INTERPRO; IPR000152; -.
INTERPRO; IPR000436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                              Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Boyidae; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 160.5; DB 6; Length 2394; 25.5%; Pred. No. 2.4e-06;
                                                                                                                                                                                      Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
VERSICAN V1 SPLICE-VARIANT.
W; B82A3E10FC5BD990 CRC64;
                                                              01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) VERSICAN VI SPLICE-VARIANT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRODOILO; EGRBLOOD.
PROSITE; PRODOILO; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PRODOIZ; EGF_1; UNKNOWN_2.
PROSITE; PROSITE; PSO1186; EGF_2; 1.
PROSITE; PSO1186; EGF_2; 1.
PROSITE; PSO1187; EGF_CA; 1.
PROSITE; PSO1241; LINK; 2.
PROSITE; PSO041; C_TYPE_LECTIN_2; 1.
PROSITE; PSO041; C_TYPE_LECTIN_2; 1.
                                  2394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Glycoprotein; EGF-like domain.
                                                        Created)
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-98288320; PubMed=9624174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261886 MW;
                                                                                                                                                                                                                                                                                             INTERPRO; IPRO00561; --
INTERPRO; IPR001304; --
INTERPRO; IPR001304; --
INTERPRO; IPR001438; --
INTERPRO; IPR001438; --
INTERPRO; IPR001801; --
FRAM; PF00008; --
PFAM; PF00008; --
PFAM; PF00004; --
PFAM; PF00004; --
PFAM; PF00019; Id; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                  PRELIMINARY;
                                                      01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                      INTERPRO; IPR000538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 2394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                   Zimmermann D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                 077610
            RESULT 11
077610
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Matches
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57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
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"Versican V2 is a major extracellular matrix component of the mature
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Sukaryota; Metazoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
368 DEPCSEETDPEH-----EECANATD
                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 15, Last anotation update)
01-CCT-2000 (TrEMBLRel. 15, Last anotation update)
LARGE AGGREGATING CARTILAGE PROTEOGLYCAN CORE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishimura M., Noshiro M., Kawamoto T., Nakamasu K., Hamada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kato Y.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB004812; BAA20524.1;
HSSP; P98066; 175G.
INTERPRO; IPRO03538; -.
INTERPRO; IPRO03006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44EA35FA92CEB8CC CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VERSICAN V3 SPLICE-VARIANT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 153; DB 6;
Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AFASONC---GSGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERAM; PF00047; 1g; 1.
PFAM; PF00193; X1ink; 1.
PRINTS; PR01265; LINKMODULE.
PROSITE; PS00290; IG_MIC; UNKNOWN_1.
PROSITE; PS01241; LINK; 1.
                                                                285 -TLEWDICASNGITHVISRXLKAPPA 309
                                                                                                       | : | | | | 410 VTTTPSVQYING-KHVVTTVPKDPEA 434
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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51 QDT---TVG--VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 QDTVSLTVEGVVFHYRAATSRYTLNFEMAQKACVDIGAVIATPEQLHAAYEDGFEQCDAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-98288320; PubMed-9624174; Schmalter K.H., Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H., Schmalfeldt M., Dours-Zimmermann D.R.; "Versican D.R.; "Versican V2 is a major extracellular matrix component of the mature bovine brain."; J. Blol. Chem. 273:15758-15764(1998).
EMBL; AF060456; AAC24358.1; -.
                                      Schmalfeldt M., Dours-Zinmermann M.T., Winterhalter K.H., Zinmermann D.R.;
Zinmermann D.R.;
Wersican V2 is a major extracellular matrix component of the mature bovine brain.";
J. Balol. Chem. 273:15758-15764 (1998).
EMBL; AF060458; AAC24360.1;
HSSP; P01132; 1EGF.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 20 POTENTIAL.
21 1643 VERSICAN V2 SPLICE-VARIANT.
1643 Aa; 182894 MW; A6F2BFC3A3DEF80A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 WLETGRVAYPTAFASQNCGS---GVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
VERSICAN VO SPLICE-VARIANT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 151.5; DB 6;
; Pred. No. 1.1e-05;
13; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00010; EGFBLOOD.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS001186; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01147; LINK; 2.
PROSITE; PS50141; LINK; 2.
PRODOM; PD000918; 7; 2.
Signal; Glycoprotein; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 3381 AA
                      WEDLINE=98288320; PubMed=9624174;
                                                                                                                                                                                                                                INTERPRO; IPRO00538; -.
INTERPRO; IPR000561; -.
INTERPRO; IPR000742; -.
INTERPRO; IPR001438; -.
INTERPRO; IPR001438; -.
INTERPRO; IPR001881; -.
INTERPRO; IPR001881; -.
PFAM; PF00008; EGF; 2.
PFAM; PF00008; EGF; 2.
PFAM; PF00047; ig; 1.
PFAM; PF00084; sushi; 1.
PFAM; PF00193; X11nk; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.2%;
Best Local Similarity 36.8%;
Matches 39; Conservative 13
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                                                                                                                                                                                 INTERPRO; IPRO00152; -.
INTERPRO; IPRO00436; -.
INTERPRO; IPRO00538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 QDT---TVG--VFHLRSPLGQYKLJFDKAREACANEAATMATYNQLSYXQKAKYHLCSAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 WLSDQTVRYPIRVPREGCYGDMMGKEGVRTYGFRA-PHETYDVYCY------VDHL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 DGDVFH-----ITAPNKFTFEEAGEECKTQDARLATVGELQAAWRNGFDRCDYGWL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 LDASVRHPVTVARAQCGGGLLGVRTLYRFENQTGFPTPDSRFDAYCFKRPDRCKMNPCLN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 WLETGRVAYPTAFASQNCGS---GVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 -GDGFSYSGNLLQVLMSFPSLTNFLTEVLAYSNSSAR--------GRAFLEHL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 TDLSIRG--TLEXPQNSG--LG-----ENE----TLSGRDIEHHLANVSMFFYNDLVN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             077611 PRELIMINARY; PRT; 1643 AA.
077611;
077611;
01-NOV-1998 (TREMBLrel. 08, Created)
01-NOV-1998 (TREMBLrel. 18, Last sequence update)
01-OCT-2000 (TREMBLREL. 15, Last annotation update)
VERSICAN V2 SPLICE-VARIANT PRECURSOR.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 GTTLQTRLGSKLLITDRQDPLHPTET --- - RCVDG --- - RDTLEWDICASN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.2%; Score 153; DB 6; Length 656; Best Local Similarity 26.8%; Pred. No. 2.3e-06; Matches 78; Conservative 26; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 POTENTIAL.
556 VERSICAN V3 SPLICE-VARIANT
74793 MW; F8FE153BD10C7AB9 CRC64;
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SEQUENCE 656 AA;
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SEQUENCE FROM N.A.
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  bovine brain.";
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DR HYSEP, PO1132; IEGEF.

DR INTERPRO; IPRO00152; --

DR INTERPRO; IPRO00153; --

DR INTERPRO; IPRO00153; --

DR INTERPRO; IPRO00153; --

DR INTERPRO; IPRO00134; --

DR PEAM; PFO0009; EGFF; 2.

DR PEAM; PFO00181; --

DR PROSITE; PSO01186; --

DR PROSITE; PSO0118
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Search completed: April 4, 2001, 13:06:28 Job time: 147 sec Netson and

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

April 4, 2001, 13:04:21; search time 11.97 Seconds (without alignments) 952.365 Million cell updates/sec Run on:

US-09-466-778-11 1857 1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

88757 seqs, 32294092 residues Searched: 88757 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P98065 Oryctolagus P98065 Oryctolagus P98066 homo sapien P07899 gallus gall P07899 rattus norv P13608 bos taurus P03994 rattus norv Q9qup5 mus musculu Q28381 equus cabal P5552 bos taurus P07354 gallus gall Q61282 mus musculu P10815 homo sapien P10815 homo sapien P10815 homo sapien P5606 mus musculu P5506 rattus norv P5506 rattus norv P5506 rattus norv Q28670 oryctolagus Q28674 arttestulus Q60505 gallus gall Q61656 mus musculu P13611 homo sapien P15379 mus musculu Q28884 canis famil
SUMMARIES	TSGE_RABIT TSGE_HUMAN PGCA_RAT PGCA_RAT PLK_MOUSE PLK_MOUSE PLK_HORSE PLK_HUMAN PLK_HUMAN PLK_HUMAN PCCA_HUMAN PCCA_HUMAN PCCA_HUMAN PCCA_HUMAN PCCA_HUMAN PCCA_RAT PCA_RAT PCA_R
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% Query Match	111 44000000000000000000000000000000000
Score	11
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P26051 rattus norv	P24014 drosophila	P35556 homo sapien	P21849 giardia lam	Q29423 bos taurus	011780 sus scrofa	Q61483 mus musculu	Q14112 homo sapien	000548 homo sapien	P10493 mus musculu	P14745 papio hamad	088322 mus musculu
CD44_RAT	SLIT_DROME	FBN2_HUMAN	TSA4_GIALA	CD44_BOVIN	BGH3_PIG	DLL1_MOUSE	NID2_HUMAN	DLL1_HUMAN	NIDO_MOUSE	CD44_PAPHA	NID2_MOUSE
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97.5	97.5	6	96	95.5	95.5	94.5	94.5	93.5	93	92.5	92.5
34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

PRT; 276 AA.	ed) acuence update) annotation update) iible Profein TSG-6 Precursor (HYALURONATE-	PS4. us. (Rabbit). Chradata, Craniata; Vertebrata; Euteleostomi; Lagomorpas Leporidas: Orvotolagus.		um and growth factor-inducible gene in $;993)$ .	90;	P., Liau G., 268:21453-21453(1993).  JOL. Chem. 268:21453-21453(1993).  FUNCTION: POSSIBLY INVOLVED IN CELL-CELL AND CELL-MATRIX INTERACTIONS DURING INPLAMMATION AND TUMORGENESIS.	AR SMOOTH MUSCLE CELLS. OWTH FACTOR. K DOMAIN.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation	ere are no restrict as its content is . Usage by and fo http://www.isb-sib		rotein. POTENTIAL. TUMR NECROSIS FACTOR-INDUCIBLE PROTEIN	1557°. LINK. CUB.
STANDARD;	01-FEB-1996 (Rel. 33, Created) 15-DEC-1996 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) TUMOR NECROSIS, FRATOR-INDUCIBLE PROFEIN TSG-6 BINDING PROFEIN PS4).	OR TSG6 OR PS4.  Ogus cuniculus (Rabbit; a; Metazoa; Chordata;	[1] SEQUENCE FROM N.A. STRAIN-NEW ZEALLAND WHITE; MEDLINE-93252803, Pubmed-8098034	<pre>Feng P., Liau G.; "Identification of a novel serum a "vacular smooth muscle cells."; J. Biol. Chem. 268:9387-9392(1993)</pre>	[2] ERRATUM. MEDLINE-94012707; PubMed-8407990	Feng P., Liau G.;  J. Biol. Chem. 268:21453-21453(1993).  -!- FUNCTION: POSSIBLY INVOLVED IN CELL-CELL AND CELL INTERACTIONS DURING INFLAMMATION AND TUMORGENESIS	-:- TISSUB SPECIFICITY: VASCULAR SMOOTH MUSCLE CELLS:- DEVELOPMENTAL STAGE: FETAL:- INDUCTION: BY SERUM AND GROWTH FACTOR:- SIMILARITY: CONTAINS I LINK DOMAIN:- STATIARITY: CONTAINS I LINK DOMAIN.	This SWISS-PROT entry is copyr between the Swiss Institute o	ppean Bioinformatics non-profit institu and this statement requires a license an email to license@	M86381; P P98066; 3 PRO; IPROC PRO; IPROC PFO0431;	Alink; 1. 10; CUB; 1. 11; LINK; 1. Signal; Glycop 19 276	DOMAIN 53 128 L DOMAIN 135 247 C
T AC ID		00000	RA RA	RT RT	R R P	3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	88888	8888	888888	S A B B B B B B B B B B B B B B B B B B	DR DR FT	444

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-FIBROBLAST:
MEDIL/RE-921293; PubMed=1730767;
MEDIL/RE-921293; PubMed=1730767;
Lee T.H. Wissiewski H.-G., Vilcek J.;
Lee T.H. Wissiewski H.-G., Vilcek J.;
A novel secretory tumor necrosis factor-inducible protein (TSG-6) is a member of the family of hyaluronate binding proteins, closely Trelated to the adhesion receptor CD44.";
J. Cell Biol. 116:545-557(1992).
                                                                                                                                                                                                     DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE-
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                     32 EQAAGVYHREARSGKYKLIYAEAKAVCEFEGGRLATYKQLEAARKIGFHVCAAGWMAKGR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 36-133.
MEDILINE-56390850, Pubmed-8797823;
Kohda D., Morton C.J., Parkar A.A., Hatanaka H., Inagaki F.M.,
Campbell I.D., Day A.J.;
Campbell I.D., Day A.J.;
Solution structure of the link module: a hyaluronan-binding domain
involved in extracellular matrix stability and cell migration.";
Cell 86:767-775(1996).
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
FY SIMILARITY.
N LINKED (GLORAC. . .) (POTENTIAL).
N LINKED (GLORAC. . .) (FOTENTIAL).
W; 3BDCSD9A24B2F75A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                             (POTENTIAL).
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-1- FUNCTION: POSSIBLY INVOLVED IN CELL-CELL AND CELL-MATRIX
INTERACTIONS DURING INFLAMMATION AND TUMORGENESIS.
                                                                                                                                       14.2%; Score 264; DB 1; Length 276; 43.3%; Pred. No. 2.5e-16; Live 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                 112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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-i- SIMILARITY: CONTAINS 1 LINK DOMAIN.
-i- SIMILARITY: CONTAINS 1 CUB DOMAIN.
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                                                                                             MM;
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                                                                                                                                                      1 Similarity 43.3% 45; Conservative
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INTERPRO: IPR000859; ...
PFAM; PF00431; CUB; 1.
PFAM F00193; Xlink; 1.
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   58
82
135
188
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258
276 AA;
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TNFAIP6 OR TSG6.
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P98066;
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Best Local S
Matches 45
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                                                                               CARBOHYD
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PGCA_CHICK STANDARD; PRT; 2109 AA.
P07898; Q90991; Q90820; C091047; Q90810;
01-AUG-1988 (Rel. 08, Created)
01-NVV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                              52 DITVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                    TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6.
LINK.
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                                                                                                                                                                                                                                                                                                                               MEDLINE=94043149; PubMed=8226878;
Li H., Schwartz N.B., Vertel B.M.;
"cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) uprotein and identification of a stop codon in the aggrecan gene associated with the chondrodystrophy, nanomelia.";
J. Biol. Chem. 268:23504-23511(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.; "Chick cartilage chondroitin sulfate proteoglycan core protein. Nucleotide sequence of cDNA clone and localization of the S103L
                                                                                                                                                                           . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chandrasekaran L., Tanzer M.L.;
"Molecular cloning of chicken aggrecan. Structural analyses.";
Biochem. J. 288:903-910(1992).
                                                                                                                                                                                                                                                    Length 277;
                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                             LINKED (GLCNAC. . .) (Po 4DB3AEB4AC52B880 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion; Signal; Glycoprotein; 3D-structure.
SIGNAL 1 19 POTENTIAL.
CHAIN 20 277 TUMOR NECROSIS FACTOR
                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                    14.1%; Score 262; DB 1; 43.3%; Pred. No. 3.7e-16; tive 16; Mismatches 43;
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SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 265:12088-12097(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=CARTILAGE;
MEDLINE=93111968; Pubmed=1339285;
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MEDLINE=90307744; Pubmed=1694853;
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   CUB; 1.
                 LINK; 1
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277 AA;
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PROSITE; PS01180;
PROSITE; PS01241;
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DR PFAM; PF00008; EGF; 1.

DR PFAM; PF00008; EGF; 1.

DR PFAM; PF00008; Lectin_c; 1.

DR PFAM; PF000084; sushi; 1.

DR PFOSITE; PS000010; ASC_HINDOXYL; 1.

PROSITE; PS010107; ASC_HINDOXYL; 1.

PROSITE; PS01021; EGF_CA; 1.

NR PROSITE; PS01041; LINK; 4.

NR PROSITE; PS00041; C_TYPE_LECTIN_1; 1.

NR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

NR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

NR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

NR EGF-like domain; Alternative Splicing; Repeat; Immunoglobulin domain.

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T SIGNAL.
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IG-LIKE V-TYPE DOMAIN.
LINK 2.
LINK 2.
LINK 3.
LINK 3.
LINK 4.
19 X 20 AA TANDEM-REPEAT.
EGF-LIKE.
C-TYPE LECTIN.
SUSHI.
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| G1-8. |
| G1-8. |
| G2-8. |
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| G2-8. |
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| C3-1. |
| C3-1. |
| G3-8. |
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G -> D (IN REF. 3).

P -> P (IN REF. 3).

A -> P (IN REF. 3).

VT -> PA (IN REF. 2).

E -> D (IN REF. 2).

I -> T (IN REF. 5).

T -> V (IN REF. 5).

E -> A (IN REF. 3).

E -> G (IN REF. 3).

E -> G (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).

DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO DOMAIN: TWO GLOBULAR PROTEOGLYCAN, WHILE ANOTHER GLOBULAR RESCHON, G3, MAKES UP THE COOH TERNINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISCLIFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAINS, N-LIKED AND C-LINKED OLIGOSACCHARIDES.

DISEASE: DEFECTS IN AGC1 IS THE CAUSE OF NANOMELIA, A LETHAL CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT CHONDEODYSTROPHY) CHRACTERIZED BY SHORTENED AND MALFORNED LIMBS. AGGRECAN IS TRUNCATED AT IS C-TERMINAL IN THE CS-2 BINDING DOMAIN AND IS NOT ANYMORE SECRETED FROM THE CHONDROCYTES.

SIMILARITY: CONTAINS 1 ENDOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86259736; PubMed-3466082;
Sai S., Tanaka T., Kosher R.A., Tanzer M.L.;
Sai S., Tanaka T., Kosher R.A., Tanzer M.L.;
Sai S., Tanaka T., Kosher R.A., Tanzer M.L.;
Cloning and sequence analysis of a partial cDNA for chicken
cartilage proteoglycan core protein.";
Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).
-!- FUNCTION: THIS PROFEGGLYCAN IS A MAJOR PUNCTION OF THIS PROTEIN
MATRIX OF CARTILAGENOUS TISSUES. A MAJOR PUNCTION OF THIS PROTEIN
IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO
HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A
REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.
-!- SUBCELLIULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                          SEQUENCE OF 1894-2109 FROM N.A.
MEDLINE-899008500; PubMed-3170613;
Tanaka T., Har-El R., Tanzer M.L.;
"Partial structure of the gene for chicken cartilage proteoglycan
                                                         SEQUENCE OF 1492-1610 FROM N.A.
STRAIN-WHITE LEGHORN: TISSUE-CHONDROCYTES;
MEDLINE-9513519; PubMed=7827752;
Primorac D., Stover M.L., Clark S.H., Rowe D.W.;
"Molecular basis of nanomelia, a heritable chondrodystrophy of
                                                                                                                                                                                                                                                                                                                                                                                                                    core protein.";
J. Biol. Chem. 263:15831-15835(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, L21913; AAB19128.1; -.
EMBL, M38187; AAA48731.1; -.
EMBL, M88101; -; NOT_ANNOTATED_CDS.
EMBL, S74656; AAC60751.1; -.
EMBL, S74656; AAC60751.1; -.
EMBL, M3993; AAA48720.1; -.
EMBL, M13993; AAA48720.1; -.
                                                                                                                                                                                                                                          Matrix Biol. 14:297-305(1994).
      Biochem. J. 296:885-887(1993).
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IPR000538;
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IPR001304;
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01-NOV-1997 (Rel. 35, Last annotation update)
AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE
PROTEIN) (CSPCP).
                                                                                                                                                SRARPNCGGNLVGVRTVYLNPANQTGYPHPSSRYDAICYSGDDFEALVPGLFTDEVGTEL 367
                                                                                                                                                                                                                     194 QCDAGWLADQTVRYPIHLPRERCYGDKDEFPGVRTYGVRETDETYDVYCYAEQMQGK--- 250
                                                                                                     VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                              117 AFASQNCGSGVVGI--VDYGPR----PNKSEMWDVFCYRMKDVNC-----TXKVG-YV 162
                                                                                                                                                                         GDGFSY-----SGNLLQVLMSFPSLTNFL, 186
                                                                                                                                                                                         368 GSAFTIQTVTQTEVELPLPRNVTEEEARGSIATLEPMEITATATELYEAFTVLPDL--FA 425
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                  10 ECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHA-------DAKCVDLHFQDTTVG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3,
                                                                                                                                                                                                                                                                                                                                                                                                                           Doege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;
Complete primary structure of the rat cartilage proteoglycan core
protein deduced from CDNA clones.";
J. Biol. Chem. 262:17757-17767(1987).
                                                  98;
                                   Length 2109;
                                 'Match 9.4%; Score 175; DB 1; Length 21
Local Similarity 23.4%; Pred. No. 2.4e-07;
les 75; Conservative 31; Mismatches 116; Indels
                                                                                                                                                                                                          187 TEVLAYSNSSARGRAFLEHLTDL-----SIRGTLFXPQNSGLGE---
-> S (IN REF. 6).
7F824FD5B3A2ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hassell J.R., Yamada
                                                                                                                                                                                                                                                                                                       PRT; 2124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doege K., Sasaki M., Horigan E., Has
J. Biol. Chem. 263:10040-10040(1988)
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88087070; Pubmed=3693370;
88 F ->
223492 MW;
                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                      483 TPGLESASPFTIEDHLVQVT 502
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                                                                                                                                                                                                                                                                                                       STANDARD;
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Rattus norvegicus (Rat).
1988
         AA;
1988

    SIMILARITY).

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CONFLICT
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P07897;
                                 Query Match
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                                                                                                                           -i- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.
-i- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 4 LINK DOMAIN.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-i- SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
-i- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROFEOGLYCAN FAMILY.
MAKES UP THE COOH TERMINUS. GI CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREED DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, MOTIFS. GZ IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITH SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
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PFAM: PF00193; X11nk; 4.

PFAM: PF00064; sush1; 1.

PROSITE; PS00290; IC_MHC; 1.

PROSITE; PS01241; IJNK; 4.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

Glycoprotein; Cartliage; Proteoglycan; Lectin; Signal; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGRECAN CORE PROTEIN
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C-TYPE LECTIN.
SUSHI.
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G1-B.
G1-B'.
G2-B.
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EMBL; J03485; AAA21000.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A23835; A23835.
PIR; A28452; A28452.
HSSP, P98665; ITSC.
INTERPRO; IPRO00436; ..
INTERPRO; IPRO004455; ..
INTERPRO; IPRO005495; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
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DOMAIN
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                                                                                                                                                                                                                                                                                                      PGCA_BOVIN STANDARD; PRT; 2364 AA.
P13608; Q28159; P79117;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteoglycan
                                                                                                                                     57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                117 AFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLL 173
                                                                                                                                                          488 VFHYRPGSTRYSLTFEEAQQACIRTGAAJASPEQLQAAYEAGYEQCDAGWLQDQTVRYPI 547
                                                                                                                32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
MEDLINE-85027710; PubMed=6489519;
MEDLINE-85027710: PubMed=6489519;
MEDLINE-85027710: PubMed=6489519;
"Sequence data concerning the protein core of the cartilage proteoglycan monomers. Characterization of a sequence allowing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a cDNA clone, contains numerous Ser-Gly sequences arranged in homologous repeats.";
Biochem. J. 243:255-259(1987).
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like
domains in aggrecans of different species. Evidence for a novel
                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
  (POTENTIAL)
                                                                                       ; Score 171; DB 1; Length 2124;
; Pred. No. 5.6e-07;
24; Mismatches 65; Indels 33
                                                                                                                                                                                                                             174 QVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGL 223
                                                                                                                                                                                                                                          SEQUENCE OF 563-1056 FROM N.A.
MEDLINE-89380219; PubMed-2528543;
Antonsson P., Heineqaard D., Oldberg A.;
The keratan sulfate-enriched region of bovine cartilage consists of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173(1989).
                                                         E30BBE61593A34B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A. MEDLINE-87270630; PubMed-3111460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 268:17377-17383(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93352525; PubMed=8349621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2114-2150 FROM N.A.
                                                                                         9.2%;
                                                         221117
                                                                                         Query Match 9.2%
Best Local Similarity 28.8%
Matches 49; Conservative
  333
387
611
667
1842
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                        2124 AA;
                                                                                                                                                                                                                                                                                                                                                                                               taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                         PROTEIN) (CSPCP).
  333
387
611
667
1842
                       CARBOHYD
CARBOHYD
                                               CARBOHYD
                                                         SEQUENCE
  CARBOHYD
              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).

DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE ANINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE C-TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B, MOTIFS. G2 IS SIMILAR TO G1. THE KERNTAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2 AND G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS LELL, 206:73-77(1986).

-!- FUNCTION: THIS PROTEGGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR

-!- FUNCTION: THIS PROTEGGLYCAN IS A MAJOR COMPONENT OF THIS PROTEIN

IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO

HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A

REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

-!- SUBCELLULAR LOCATION: SECRETED: EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADULT AND FETAL BOVINE PROTEOGLYCANS.
SIMILARITY: CONTAINS 1 INMUNOCIOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 INMUNOCIOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LEGETIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LEGETIN FEPRAL.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O-LINKED (ABOUT 40) OLIGOSACCHARIDES.
PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
                                                                                                                                                              Perin J.P., Bonnet F., Jolles P.; "Structural relationship between link proteins and proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
synthesis of an oligonucleotide probe."; FEBS Lett. 176:37-42(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L07053; -; NOT_ANNÓTATED_CDS.
PIR; A27752; A27752.
PIR; A29164; A29164.
PIR; B29164; B29164.
PIR; E20164; E29164.
PIR; G27751; G27751.
HSSP; P00740; 11XA.
                                                                                                                                   MEDLINE=87005253; PubMed=3530809;
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INTERPRO; IPR000436; -.
INTERPRO; IPR000561; -.
INTERPRO; IPR001304; -.
INTERPRO; IPR001304; -.
FYAM; PF00008; EGF; 1.
PFAM; PF000193; X1ink; 4.
PFAM; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U76615; AAB38524.1;
                                                                                                PARTIAL SEQUENCE.
                                                                                                                                                                                                                                    monomers.";
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MEDLINE=86140139; PubMed=2419334;
Neame P.J., Christner J.E., Baker J.R.;
"The primary structure of link protein from rat chondrosarcoma proteoglycan aggregate.";
J. Biol. Chem. 261:5319-335(1986).
-i- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH
                                                                                                                          HYALDRONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LOG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHORT ISOFORM).
MISSING (IN SHORT ISOFORM)
R -> W (IN REF. 3).
23278AEA56273D6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                  EMBL, M22340; AAA41535.1; --
EMBL, M22336; AAA41535.1; JOINED.
EMBL, M22337; AAA41535.1; JOINED.
EMBL, M22339; AAA41535.1; JOINED.
EMBL, M22336; AAA41536.1; --
EMBL, M22336; AAA41536.1; JOINED.
EMBL, M22339; AAA41536.1; JOINED.
PIR; AQ2869; LKRTZ.
HSSP; P98066; LTSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SGVVGIVDYGPRPNKSEMWDVFCY 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERRECO; INTERPRO; INTERPRO; IPROGOGS38; -... INTERPRO; IPROGOGO; -... PFAM; PFOOLO47; IIIn; 2... PFAM; PFOOLO47; IG; 1... PROSITE; PSO1241; LINK; 2...
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Best Local Similarity 30.8'
Matches 45; Conservative
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                  OF 16-354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
LINK 3.

LINK 4.

23 X 6 AA APPROXIMATE TANDEM REPEATS OF
E-[E1] - P-F-P-S.

CS-2.
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                                                                                             EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88198139; PubMed-2452158;
Rhodes C., Doege K., Sasaki M., Yamada Y.;
"Alternative splicing generates two different mRNA species for rat
link protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1986 (Rel. 02, Created)
1-FFB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDILTHE-86233141, PubMed-3459153;
Dogge K., Hassell J.K., Caterson B., Yamada Y.;
"Link protedn cDNA sequence reveals a tandemly repeated protein
                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; Score 170; DB 1; Length 2364;
88.9%; Pred. No. 7.8e-07;
Ive 12; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ING (IN ISOFORM 2).
6FF83763420C3D4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure.";
Proc. Natl. Acad. Sci. U.S.A. 83:3761-3765(1986).
                                                                                                                                                           N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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N-LINKED (GLCNAC...
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BY SIMILARITY.
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                                                                                 C-TYPE
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Matches 37; Conservative
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ABGOPELLYARDPTAFGSG
IHKIRIKWTKLTSDY -> DCTAFWKLIEGRORSSASPVG
ILTMPCCFPWRKHYTWKGIKSLKLPSLAISDRTS (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Connective tissue; Extracellular matrix; Cartilage; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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PLK\_MOUSE

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                                      65 GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from complementary DNA.";
Am. J. Vet. Res. 56:959-965(1995).
-!- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete primary sequence of equine cartilage link protein deduced
                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEOGLYCAN LINK PROTEIN.
PROTEOGLYCAN LINK PROTEIN.
LINK 1.
LINK 2.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MM; D015CB07016C7172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P98066; 1TSG.
INTERPRO. IPRO0306; -.
INTERPRO. IPRO0306; -.
PFAM; PF00193; X1ink; 2.
PFAM; PF00047; 4g; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 166.5; DB 1;
Pred. No. 1.5e-07;
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30.1%; Pred. No. 1...
22; Mismatches
                                                                                                                                                                                                                                354 AA.
                                                                                                                      230 GONTVPGVRNYGFWDKDKSRYDVFCF 255
                                                                                            125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=CARTILAGE;
MEDLINE=96039874; Pubmed=7574168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40077 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Conservative
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dudhia J., Platt D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                        RESULT 8
PLK_HORSE
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Beier D.R., Kiss I.;
"Characterization and chromosomal location of the mouse link protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytogenet. Cell Genet. 87:75-79(1999).
-!- FUNCTION: STABILIZE THE AGREGATES OF PROTEOGLYCAN MONOMERS WITH
-!- HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
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                                                                                                                                                                    01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01265; LINKMODULE.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Connective Issue; Extracellular matrix; Cartilage;
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKED (GLCNAC. . .) (POTENTIAL). 3FB4B8F30E28C9F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 169.5; DB 1;
30.8%; Pred. No. 8.4e-08;
ive 20; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINK 1.
LINK 2.
LINK 2.
N-LINKED GECNAC.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED GECNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                              356 AA.
228 GQNTVPGVRNYGFWDKDKSRYDVFCF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF137278; AAF24166.1; -.
EMBL; AF137275; AAF24166.1; JOINED.
EMBL; AF137276; AAF24166.1; JOINED.
EMBL; AF137277; AAF24166.1; JOINED.
EMBL; AF139572; AAF24977.1; -.
                                                                                                                                                  01-OCT-2000 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                              STANDARD;
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INTERPRO; IPR000538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; ig; 1.
PFAM; PF00193; Xlink; 2.
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58
356 AA;
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=129/SV;
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41
178
276
58
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183
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                                                                                                            PLK_MOUSE
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Best Local S:
Matches 45;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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Gaps

29;

51; Indels

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--EDDTAVVALDLQGV---VFPYFPRL 167

|::||| |:|| 135 GRYKCE----VIEGL----

65

168 GRYNLNFHEAQQACLDQDAVIASFDQLYDAWRSGLDWCNAGWLSDGSVQYPITKPREPCG 227

GOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG

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 ---EDDTAVVALDLQGV---VFPYFPRL 167
                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                   Hering T.M., Kollar J., Huynh T.D., Sandell L.J.;

"Bowine chondrocyte link protein cDNA sequence: interspecies

"Bowine chondrocyte link protein cDNA sequence: interspecies
conservation of primary structure and mRNA untranslated regions.";

conp. Biochem. Physiol. 1128:197-203(1995).

-!- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLOLAR CARTILAGE MATRIX.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                        GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO1241; LINK; 2.
Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
PROPEP 1 15 BY STMITARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
PROTEGGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
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SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                               125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                             228 GONTVPGVRNYGFWDKEKSRYDVFCF 253
                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=CARTILAGE;
MEDLINE=96043243; PubMed=7584851;
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BY
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|::||| | :||
135 GRYKCE----VIEGL----
                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3354
2253
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3252
3253
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                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
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354 AA;
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                                                                                                                                                                                                  PLK_BOVIN
P55252;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
MEDLINE-87317659; PubMed-3476955;
Kiss I., Deak F., Mestric S., Delius H., Soos J., Dekany K.,
Argraves W.S., Sparks K.J., Goetinck P.F.;
"Structure of the chicken link protein gene: exons correlate with the
                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 84:6399-6403(1987).
-!- FUNCTION: STABILIZE THE AGGREGATES OF PROTEGGLYCAN MONOMERS WITH
HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                               01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                      'Complete amino acid sequence of chicken cartilage link protein
                                                                                                                                                                                                                                                                                                                                                                                                  Deak F., Kiss I., Sparks K.J., Argraves W.S., Hampikian G.,
Goetinck P.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEOGLYCAN LINK PROTEIN. IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         deduced from cDNA clones.";
Proc. Natl. Acad. Sci. U.S.A. 83:3766-3770(1986).
                                                                                                                              355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=EMBRYONIC STERNAL CARTILAGE;
MEDLINE=86233315; Pubmed=3459154;
125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                 228 GONTVPGVRNYGFWDKDKSRYDVFCF 253
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M35038; AAA48941.1; -.
EMBL; M35035; AAA48941.1; JOINED.
EMBL; M35036; AAA48941.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M35036; AAA48941.1; JOINED.
                                                                                                                                                              01-APR-1988 (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01241; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M13212; AAA48940.1;
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000538; -. INTERPRO; IPR003006; -. PFAM; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A24881; LKCH.
PIR; A28305; A28305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00047; ig; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P98066; 1TSG
                                                                                                                          PLK_CHICK
P07354;
                                                                                                                                                                                                                                                                                                               Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
```

4;

Gaps

29;

DB 1; Length 354; 51; Indels

8.9%; Score 165.5; DB 130.1%; Pred. No. 1.9e-07; Live 22; Mismatches 51

44; . Conservative

Similarity

Query Match

Best Local

Matches

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Page

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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).

DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEGGIVCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISGLIFIDE. BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULEATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEOGLICAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE. SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q61282; Q64021;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE
PROTEIN) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in
                                                                                                                                                                                                                                                                                                                                                                           64 LGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNC 123
                                                                                                                                                                                                                                                                                                                                                                                                 136 GRYKCE----VIEGL------GVVFPYSPR 167
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                  5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSP- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
LINK 1.

LINK 2.

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete coding sequence, deduced primary structure, chromosomal localization, and structural analysis of murine aggrecan."; Genomics 22:364-371(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-CARTILAGE;
MEDLINE-95104647; Pubmed-7806222;
WALOZ E., Deak F., Erhardt P., Coulter S.N., Fueloep C., Horvath
Doege K.J., Glant T.T.;
                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                             Length 355;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                      2581CAE22158B60F CRC64;
                                                                                                                                                                                                                           Score 165.5; DB 1;
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2132 AA
                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    G--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | |: : | | : : | | GGKNTVPGVRNYGFWDKERSRYDVFCF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95004579; PubMed=7920633;
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                                                                                                                                                                                                                           8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the aggrecan gene.";
Nat. Genet. 7:154-157(1994)
                                                                                                                                                                      40533
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
 254
351
140
140
225
227
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326
21
56
                                                                                                                              21
56
355 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                44;
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ID PGCA_MOUSE
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                                                                                                                                                    CARBOHYD
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   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               168
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AND G3.

THE CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.

DISEASE: DEFECTS IN ACTI ARE THE CAUSE OF CARTILAGE MATRIX DEFICIENCY (CMD), AN AUTOSOMAL RECESSIVE SYNDROME CHARACTERIZED BY CLEFT PALATE, SHORT LIMBS, TAIL AND SNOUT. MUTATION IN STRAIN CMD CAUSES ABSENCE OF AGGRECAN BY TRUNCATION OF THE PROTEIN (MUTATION IN THE G1 DOMAIN).
                                                                                                                                  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 4 LINK DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) REPERT.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00193; Xlink; 4.
PFAM; PF001639; Alink; 4.
PFAM; PF00064; Sussh; 1.
PROSITE; PS01240; IG_MHC; 1.
PROSITE; PS01241; LINK; 4.
PROSITE; PS00415; C_TYPE_LECTIN_1; 1.
PROSITE; PS00415; C_TYPE_LECTIN_2; 1.
Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sushi; Stepeat; Immunoglobulin domain.
SIGNAL 1 19 POFFNTTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGRECAN CORE PROTEIN IG-LIKE V-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINK 4.
C-TYPE LECTIN.
SUSHI.
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EMBL; S73722; AAB32160.1; -.
EMBL; S73721; AAB32160.1; -.
EMBL; S73721; AAB32160.1; JOINED.
HSSP; P98066; 1TSG.
MGD; MGI:99602; AGC.
INTERPRO; IPR000436; -.
INTERPRO; IPR000436; -.
INTERPRO; IPR001304; -.
INTERPRO; IPR001304; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G1-A.
G1-B.
G1-B'
G2-B.
KS.
KS.
CS-1.
GS-1.
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581
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175
199
2273
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1922
1950
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                                                                                                                                                                                                                                                 117 AFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CRTL1)
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterization of the promoter for the rat and human link protein
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91232964; Pubmed-2030970;
Rhodes C., Savagner P., Line S., Sasaki M., Chirigos M., Doege K.,
Yamada Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 11, Created)
1-JUL-1999 (Rel. 14, Last sequence update)
1-NOV-1997 (Rel. 35, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91139126; PubMed-2286376; Osborne-Lawrence S.L., Sinclair A.K., Hicks R.C., Lacey S.W., Eddy R.L. Jr., Byers M.G., Shows T.B., Duby A.D.; "Complete amino acid sequence of human cartilage link protein (CF deduced from cDNA clones and chromosomal assignment of the gene." Genomics 8:562-567(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 19:1933-1939(1991).
-I- FUNCTION: STABILIZE THE AGREGARES OF PROTEOGLYCAN MONOMERS
HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
-I-* SIMILARATY: COWTAINS I IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                   32;
                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL CELL ATTACHMENT SITE (POTENTIAL). W; 0B2BCDFC6CBDA163 CRC64;
                                                                                                                                                                    8.9%; Score 165; DB 1; Length 2132;
28.8%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                         174 QVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-ARTICULAR CHONDROCYTES;
MEDLINE-90206798; PubMed-2320422;
Dudhia J., Hardingham T.E.;
"The primary structure of human cartilage link protein.";
Nucleic Acids Res. 18:1292-1292(1990).
                                                                                                                                                                                                   66; Indels
                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dudhia J., Hardingham T.E.;
Nucleic Acids Res. 18:2214-2214(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90245703; PubMed-2336413;
                                                                                                                           .
E
                                                                                                                       222008
                                                                                                                                                                                   28.8%;
                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                           A
A
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                          611
667
1675
1171
2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLK_HUMAN
P10915;
                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                         SITE
SEQUENCE
 CARBOHYD
                             CARBOHYD
                                                                                           CARBOHYD
                                                                                                                                                                    Query Match
                                                                                                                                                                                    Best Local
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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SEQUENCE FROM N.A.

TSUSDE_LARKRYGELE CARFILLAGE CHONDROCYTES;

MEDI.NE=89293837; Pubmed=2738916;

Perkins S.J., Nealis A.S., Dudhia J., Hardingham T.E.;

Perkins S.J., Nealis A.S., Dudhia J., Hardingham T.E.;

Timmunoglobulin fold and tandem repeat structures in proteoglycan terminal domains and link protein.";

J. Mol. Biol. 206:737-753 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL
                                                                                                                                                                                                                                                                           Extracellular matrix; Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%; Score 163.5; DB 1; Length 354; 10.1%; Pred. No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN)
                                                                                                                                                                                                                                                                          Glycoprotein; Connective tissue; Extracellular matrix; Cartil
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                  PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINKED (GLCNAC. . .) (PO
315C96EC3AC2626A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 GONTVPGVRNYGFWDKDKSRYDVFCF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                            EMBL; X17405; CAA35462.1; --
EMBL; U43328; AAA85216.1; --
PIR; S14914; LKHU.
PIR; A36308; A36308.
HSSP; P98066; 1TSG.
MIM; 115435; --
INTERPRO; IPRO00538; --
INTERPRO; IPRO0066; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40165 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.1%;
                                                                                                                                                                                                                                                PFAM; PF00047; ig; 1.
PROSITE; PS01241; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Conservative
                                                                                                                                                                                                                               PFAM; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                  146
2253
2252
2252
325
325
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176
274
274
181
205
279
304
354 AA;
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Best Local Similarity
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
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DOMAIN
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EMBL, 37459; AAC60643.1; -. P.TR; SOB042; SOB042 BESP; P98066; 178G.
MMS, 155760; -. TWENDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEO0008; EGF; 1.
PF00193; Xlink; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO00436; -. INTERPRO; IPR000495; -. INTERPRO; IPR000538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO;
                                                                                                                                                                                                                                               aggrecan.
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PFAM; 1
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYALURONIC ACID IN THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH STMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRYKCE----VIEGL-----VFPYFPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGCA_HUMAN STANDARD; PRT; 2415 AA.
P16112; Q13650;
01-APR-1990 (Rel. 14, Created)
01-AVG-1992 (Rel. 23, Last sequence update)
30-AMY-2000 (Rel. 39, Last sequence update)
AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              Glycoprotein; Connective tissue; Extracellular matrix; Cartilage;
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
PROPEE
                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                        52; Indels
                                                                                                                                                                                                                                                         PROTEOGLYCAN LINK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                       68FFFB9DE51ABCC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-2162; 2201-2329 AND 2391-2415 FROM N.A.
                                                                                                                                                                                                                                                               IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 161.5; DB Pred. No. 4.3e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-CHONDROCYTES,
MEDLINE-91093289; PubMed-1985970;
Doege K.J., Sasaki M., Kimura T., Yamada Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 GONTVPGVRNYGFWDKDKSRYDVFCF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                  8.7%;
                                                                                                                                         EMBL; Y00165; CAA68358.1; -.
                                                                                                                                                   PIR; S04243; S04243.
HSSP, P98066; LTG.
INTERPO: IPR000538;
INTERPO: IPR003006; -.
PFAM: PF000193; XIInk; 2.
PFAM: PF00047; ig: 1.
PROSITE; PS01241; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                       40260
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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2553
3350
1139
2252
3256
3253
3253
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56
354 AA;
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181
205
279
304
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Best Local S:
Matches 43;
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LIKKED OLIGOSACCHARIDES.
SIMILARITY: CONTAINS 1 IMMONGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 4 LINK DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: THE THE PROTECTION, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTECCLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSIGTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G3 AND G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MACTIX BIO1. 14:323-328(1994).

-!- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTHIAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTHIAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.
-!- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
ALTERNATIVE PRODUCTS: THERE ARE AT LEAST THREE FORMS OF AGGRECAN TRANSCRIPTS GENERATED BY ALTERNATIVE EXON USAGE. THE SHORTEST AND ALSO THE MOST PREVALENT FORM, LACKS BOTH THE EGF-LIKE DOMAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1936-2415 FROM N.A. MEDIATE-8930154; PUBMed=2789216; MEDIATE-8930154; PubMed=2789216; Parlottne=84980154; Prockop D.J.; Reginato A.M., Prockop D.J.; A new epidermal growth factor-like domain in the human core protein for the large cartilage-specific proteoglycan. Evidence for allernative splicing of the domain."; J. Biol. Chem. 264:15747-15750(1989).
carillage large aggregating proteoglycan, aggrecan. Human-specific repeats, and additional alternatively spliced forms."; biol. Chem. 266:894-902(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of mammalian
                                                                                                                                                                                                                                                                                                       TISSUE=CHONDROCYTES;
Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barry F.P., Neame P.J., Sasse J., Pearson D.; "Length variation in the keratan sulfate domain
                                                                                                                                                                                                                                                           SEQUENCE OF 1778-2162 AND 2201-2415 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95128522; PubMed=7827755;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M55172; AAA62824.1; -.
EMBL; J05062; AAA35726.1; -.
EMBL; X17406; CAA35463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUSHI DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
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PFAM; PF00059; lect...

R PFAM; PF00064; sush; l.

DR PROSITE; PS01062; EGF_l; l.

DR PROSITE; PS01241; LINK; l.

DR PROSITE; PS001241; LINK; l.

DR PROSITE; PS006125; C_TYPE_LECTIN_l; l.

DR PROSITE; PS00612; C_TYPE_LECTIN_l; l.

DR PROSITE; PS50641; C_TYPE_LECTIN_l; l.

KW Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sush;

KW Glycoprotein; Alternative splicing; Repeat; Immunoglobulin domain.

SIGNAL 1 19 AGGRECAN CORE PROTEIN.

44 140 IG-LIKE V-TYPE DOMAIN.

1 247 LINK 1.

TNK 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                         12 x APPROXIMATE TANDEM REPEATS.
CS-1.
29 x APPROXIMATE TANDEM REPEATS.
CS-2.
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P (IN REF. 2 AND 3).
1288937E1B98C6B6 CRC64;
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MISSING (IN ISOFORM 3).
E -> b / TM
                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINED GLONAC...)
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                                                                                                                                                                                                                                                                                          SIMILARITY
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                                                                                                                                                                                         G1-A.
G1-B.
G1-B'
G2-B.
G2-B.
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CARBOHYD
CARBOHYD
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Ouery Match

8.7%; Score 161.5; DB 1; Length 2415;
Best Local Similarity 27.9%; Pred. No. 4.6e-06;
Matches 50; Conservative 22; Mismatches 64; Indels 43; Gaps 6;

47 DLHFQDTTVG------VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKA 97
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 28:405-410(1995).
-!- FUNCTION: MAY MODULATE NEURONAL ADHESION AND NEURITE GROWTH DURING DEVELOPMENT BY BINDING TO NEURAL CELL ADHESION MOLECULES (NG-CAM AND N-CAM). CHONDROITIN SULFATE PROTEOGLYCAN; BINDS TO HYALURONIC
"Structure and chromosomal localization of the mouse neurocan gene.";
                                                 98 KYHLCSAGWLETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCY---- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
SIMILARITY: CONTAINS 1 C-TYPE LEGEN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LEGEN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                -----RMKDV------NCTXKVGYVGDGFS-----YSGNLLQVLMSFPSLT 183
                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                   STRAIN=BALB/C; TISSUE=BRAIN; MEDLINE=96039250; PubMed=7490074; Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D. Faessler R.;
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                               PRT; 1268 AA
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                                                                                                                                                                                                                                                         01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequé
15-JUL-1998 (Rel. 36, Last annot
NEUROCAN CORE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00084; sushi; 1.
PROSITE; PS00010; ASX_HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E; PS01186; EGF_1; 3.
F; PS01187; EGF_2; 1.
F; PS01187; EGF_CA; 1.
F; PS01241; LINK; 2.
FS00615; C_TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: BRAIN
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PF00059; lectin_c; 1.
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INTERPRO; IPRO00152; -
INTERPRO; IPRO00536; -
INTERPRO; IPRO00561; -
INTERPRO; IPRO01861; -
INTERPRO; IPRO01804; -
INTERPRO; IPRO01804; -
INTERPRO; IPRO01804; -
PFAM; PFO01093; XIINK; 2.
                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                               PGCN_MOUSE
P55066;
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PGCN_MOUSE
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3; 47 DLHFQDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGW 106 7; Gaps Ouery Match 8.5%; Score 158.5; DB 1; Length 1268; Best Local Similarity 34.2%; Pred. No. 3.8e-06; Matches 41; Conservative 19; Mismatches 53; Indels 7;

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107 LETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVG 163 Д Óγ

210

q

Search completed: April 4, 2001, 13:06:41 Job time: 140 sec

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4.5	Compugen
version 4	- 2000
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

April 4, 2001, 13:03:57; Search time 17.49 Seconds (without alignments) 1370.436 Million cell updates/sec Run on:

US-09-466-778-11 1857 1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues

195891 Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_66:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		dФ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
7	1468	79.1	1069	. 2	T42681	hypothetical prote
7	264	14.2	275	~	JC6506	
ĸ	264	14.2	276	a	A47290	homolog
4	262	14.1	277	7	A41735	hyaluronate-bindin
J.	175		2109	~	150421	aggrecan precursor
9	171	•	2124	N	A28452	
7	170		2327	7	T42630	aqqrecan - bovine
80	169.5		408	Н	LKRT2	proteoglycan link
6	166.5		354	Н	S42938	proteoglycan link
10	165.5	8.9	355	Н	LKCH	proteoglycan link
11	165		2132	-	A55182	aggrecan precursor
12	163.5		354	Н	LKHU	proteoglycan link
13	161.5	8.7	354	Н	S04243	
14	161.5	•	2316	щ	A39086	aggrecan precursor
15	160		370	~	S29139	
16	158.5		1268	~	S52781	,
17	157.5		371	~	A53908	brevican precursor
18	157.5	8.5	883	7	S49126	brevican precursor
19	157.5		1257	~	S28764	neurocan precursor
20	155.5	•	912	~	A54423	brevican precursor
21	154.5		862	ď	S43922	versican - pig-tai
22	152.5		3562	7	A47171	chondroitin sulfat
23	151.5	8.2	1643	7	T14274	versican precursor
24	151.5		3381	7	T42389	versican precursor
25	150.5		883	7	S57653	brevican precursor
26	150.5		2409	П	A60979	versican precursor
27	148		2397	٦	A55535	versican precursor
28	147	7.9	378	7	146268	brevican precursor
29	139.5	•	1340	7	A39808	proteoglycan core

chondroitin sulfat	T-cell surface gly	plasma membrane gl	CD44 homolog membr	CD44R5 - human	lymphocyte surface	hypothetical prote	hypothetical prote	CD44 membrane glyc	CD44 antigen precu	C-Delta-1 - chicke	intrinsic factor-B	hypothetical prote	fibrillin-2 precur	lymphocyte surface	cell surface glyco
A55885	A35616	A34907	A37009	177371	S24240	T22674	T34513	A34424	845305	150719	T09456	T22025	A57278	A32377	G02251
7	N	~	7	7	~	~	7	7	7	7	7	7	7	7	7
113	362	358	363	395	359	1584	3507	365	351	728	3623	601	2907	294	361
9.9	0.9	5.9	5.9	5.8	5.7	5.7	5.6	5.6	5.4	5.4	5.4	5.3	5.3	5.3	5.3
122	111.5	109.5	109.5	108	106	105	104	103.5	100	99.5	99.5	66	66	86	86

# ALIGNMENTS

RESULT 1  Myoghetical protein DKF2p434E0321.1. human (fragments)  C;Species: Homo sapiens (man)  C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000  C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000  C;Date: 11-Jan-2000  R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  submitted to the Protein Sequence Database, November 1999  A;Reference number: 22233  A;Reference number: 22233  A;Accession: T42681  A;Accession: Preliminary  A;Accession: Preliminary  A;Molecule type: mRnA  A;Residues: 1870,871-1069 <aaa>  A;Residues: 1870,871-1069 <aaa>  A;Residues: adult testis; clone DKFZp434E0321  A;Rote: the cDNA sequence contains a +1 frameshift near codon 870  C;Genetics:  A;Note: DKFZp434E0321.1</aaa></aaa>	Query Match 79.1%; Score 1468; DB 2; Length 1069; Best Local Similarity 80.5%; Pred. No. 1.10-117; Matches 284; Conservative 4; Mismatches 29; Indels 36; Gaps	1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60	61 RSPLGQYKLTFDKAREACANEAATVATVNOLSYXOKAKYHLCSAGWLETGRVAYPTAFAS 120 	121 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180	181 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPONSGLGENETLSGRDIEHHLAN 240 ::	241 VSMFFYNDIVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300 	301 SRXLKAPPAPVTLXHTXLGXGIFXXIILVTGAVALAAYSVFRINBKTIGFXHF 353 
RESULT 1 142681 Charletica Charletica Charletill Charletill Accession Rhum, H.; Asbumitted the Ascession A	Query Best I Matche		7				
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RESULT 2 JC6506 tumor necrosis factor stimulated gene-6 protein - mouse

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #text_change 28-May-1999
C;Accession: A4173; D53642
A;Tele, T.H.; Wisniewski, H.G.; Vilcek, J.
A;Cell Biol. 116, 545-557, 1992
A;Title: A novel secretory tumor necrosis factor-inducible protein (TSG-6) is a member A;Reference number: A41735; MUD:92112993
A;Reference number: A41735; MUD:92112993
A;Reference number: A41735; MUD:92112993
A;Residues: 1-277 <LEE>
A;Crossion: A41735
A;Residues: 1-277 <LEE>
A;Crossion: A41735
A;Residues: 1-277 <LEE>
A;Residues: 1-277 <LEE
A;Note: sequence extracted from NCBI backbone (NCBIN:76828, NCBIP:76833)
A;Note: sequence extracted from NCBI backbone (NCBIN:76828, NCBIP:76833)
B;Note: sequence extracted from NCBI backbone (NCBIN:76828, NCBIP:76833)
A;Note: sequence extracted from NCBI backbone (NCBIN:76828, NCBIP:76833)
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable content of the sequence number: A53642; MUD:94271799
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable content special protein associated hyaluronate-binding protein repeat homology classical cylloporotein repeat homology classical status predicted <AIC
C;Superfamily: CIrClis repeat homology class
F;20-277/Product: hyaluronate-binding protein repeat homology class
F;3-128/Domain: signal sequence #status predicted (ASI)
F;3-128/Domain: clr/Cis repeat homology class
F;3-128/Domain: clr/Cis repeat homology class
F;118,258/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1:361, 'DL', 364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1602,
A; Cross-references: GB:M8H0.
A; Cross-references: GB:M9H0.
B; Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A; Title: Molecular cloning of chicken aggrecan. Structural analyses.
A; Accession: S27356; MUID: 93111968
A; Accession: S27356
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilternate names: cartilage chondroitin sulfate proteoglycan core protein Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: 10-Sep-1999 #text_change 21-Jan-2000
Cisaccession: 150421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
Rill, H.; Schwartz. NB:; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A; Fitle: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein
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A; Reference number: A48884; MUID:94043149
A; Accession: I50421
A; Astatus: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2109 < LIX
B; Chandrasekaran, L.; Tanzer, M.L.
B; Chandrasekaran, L.; Tanzer, M.L.
B; Chandrasekaran, L.; Tanzer, M.L.
A; Reference number: S39796; MUID:94107258
A; Contents: annotation; erratum
A; Accession: S39796
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.larity 43.3%; Pred. No. 4.7e-15;
Conservative 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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C; Species: Oryccolagus cuniculus (domestic rabbit)
C; Species: Oryccolagus cuniculus (domestic rabbit)
C; Date: 03-Mar-1994 **Requence_revision 07-Jul-1995 **text_change 08-Oct-1999
C; Accession: A48055; A47290
S; Freng, P.; Liau, G.
J. Biol. Chem. 266, 21453, 1993
A; Reference number: A48055; MUID: 94012707
A; Molecule type: MRNA
A; Residues: 1-276 **FENA
A; Reference number: A49055
A; Title: Identification of a novel serum and growth factor-inducible gene in vascular sm A; Reference number: A47290; MUID: 93252803
A; Title: Identification of a novel serum and growth factor-inducible gene in vascular sm A; Reference number: A47290; MUID: 93252803
A; Residues: 'MEGSNRKSQLTTEDVALDGWTCRKNSFVLTVVRTNGLYAALVSLGNRRRPGVTVQRTEGNFSSRHESCAREPALG
A; Residues: 'MEGSNRKSQLTTEDVALDGWTCRKNSFVLTVVRTNGLYAALVSLGNRRRPGVTVQRTEGNFSSRHESCAREPALG
A; Note: sequence extracted from NCBI backbone (NCBIN:131599)
A; Note: the sequence reported here was found to be artifactual, a hybrid molecule of twc c; Superfamily: CIr/Cis repeat homology cIR/C)
C; Superfamily: CIr/Cis repeat homology cIR/C)
F; 53-128/Domain: Link protein repeat homology CIR/C)
   C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JG506
R;Ruchoep, C.; Kamath, R.V.; Li, Y.; Otto, J.M.; Salustri, A.; Olsen, B.R.; Glant, T.T.;
Gane 202, 95-Ju2, 1997
A;Fitle: Coding sequence, exon-intron structure and chromosomal localization of murine: A;Reference number: JG6506, MuID:98087423
A;Accession: JG6506
A;Accession: JG6506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-275 <FVES>
A;Cross-references: GB:U83903; NID:92062474; PIDN:AAC53527.1; PID:92062475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | || VGYPIVKPGSNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKEC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 264; DB 2;
; Pred. No. 3.1e-15;
16; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%; Score 264; DB 2; 43.3%; Pred. No. 3.1e-15; iive 16; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 43.39 tes 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 45; Conserve
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Best Local Si
Matches 45;
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Nighternate names: aggreene
Nighternate names: aggreene
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: A92623; A23835; A28453; A28452
R; Boege, K; Sasaki, M; Horigan, E; Hassell, J.R.; Yamada, Y.
J; Biol. Chem. 262, 1775-17767, 1387
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein de
A;Accession: A92623
A;Molecule type: mRNA
A;Accession: A92623
A;Molecule type: mRNA
A;Residues: 1-2124 < CDDES
R; Boege, K; Sasaki, M; Horigan, E; Hassell, J.R.; Yamada, Y.
J; Biol. Chem. 263, 10040a, 1988
A;Residues: 1-3124 < CDDES
B;Doege, K; Fernandez, P; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J; Biol. Chem. 261, 8108-8111, 1986
A;Contents: annotation; revision to residue 698
A;Contents: annotation; revision to residue 698
A;Contents: 261, 8108-8111, 1986
A;Title: Partial CDNA sequence encoding a globular domain at the C terminus of the ra
A;Accession: A23835; MUID:86250698
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A: Residues: 1856-2124 < DO2>
A: Residues: 1856-2124 < DO2>
A: Cross-references: 68.M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
B: Neame, P.J.; Christner, J.E.; Baker, J.R.
J. Biol. Chem. 262, 17768-17778, 1987
A: Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-the A: Reference number: A28453; MUID:88087071
A: Reference number: A28453
A: Molecule type: protein
A: Molecule type: protein
A: Molecule type: protein
C: Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; C: Reywords: glycoprotein
C: Keywords: glycoprotein
F: 1-19/Domain: signal sequence #status predicted <SIG>
F: 20-2124/Product: proteoglycan core protein #status predicted <MAT>
E: 20-2124/Product: proteoglycan core protein #status predicted <MAT>
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F;170-247/Domain: link protein repeat homology <IMM>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;605-683/Domain: link protein repeat homology <LNK3>
F;619-2034/Domain: C-type lectin homology <LNK4>
F;2041-2097/Domain: c-type lectin homology <LCH3-
F;2041-2097/Domain: complement factor H repeat homology <FHD>
F;2041-2097
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                                                                                                                                                                         426 TSVIVETASPREENVIREEITGIWAVPEEVITSVSGTAF----TIGMAEVSSVEEAIAVTA 482
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28.8%; Pred. No. 3.7e-06;
tive 24; Mismatches 65
                                                                                    187 TEVLAYSNSSARGRAFLEHLTDL-
                                                                                                                                                                                                                                                                                                                                                                         |: | || || || 483 TPGLESASPFTIEDHLVQVT
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A; Residues: 1893-1987, %', 1989-2022 <TAN>
A; Molecule type: DNA
A; Residues: 1893-1987, %', 1989-2022 <TAN>
A; Note: the authors translated the codon TCC for residue 1787 as Phe
B; Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A; Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s
A; Reference number: 150216
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: PA', 1044-1559 <KRU>
A; Residues: PA', 1044-1559 <KRU>
A; Residues: Cham. 265, 12075-12087, 1990
A; Cross-references: GB: M38187; NID: q211685; PIDN: AAA48731.1; PID: q555441
B; Krueger Jr., R.C.: Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A; Title: Chick cartilage chondroitin sulfate proteoglycan core protein: I. Generation an A; Reference number: A37072; MuID: 90307743
A; Molecule type: MID: 90307743
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A; Accession: B3/v/z
A; Accession: B3/v/z
A; A; Accession: B3/v/z
A; Bobiccule type: protein
A; Residues: 1247-1250, 'D', 1252-1272,'X',1274-1275 < KR3>
A; Note: amino end of 75K core peptide CS-B
C; Superfamily: aggrecan; C'type lectin homology; complement factor H repeat homology; EC
C; Keywords: alternative splicing
F; 1-20/Domain: signal sequence #status predicted <SIG>F; 1-2109/Product: aggrecan #status predicted <MAT>
F; 1-2109/Product: aggrecan #status predicted <MAT>
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F; 65-346/Domain: link protein repeat homology <LNK2>
F; 537-614/Domain: link protein repeat homology <LNK3>
F; 537-614/Domain: link protein repeat homology <LNK4>
F; 635-716/Domain: EGF homology <EGF>
F; 1897-2017/Domain: C-type lectin homology <LCH>
F; 1897-2017/Domain: C-type lectin homology <LH>
F; 1897-2017/Domain: C-type lectin homology <LH

F; 1897-2017/D
A: Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1549, 'T', A: Cross-references: EMBL:M88101

A:Cross-references: EMBL:M88101

Froc. Natl. Acad. Sci. U.S.A. 83, 2081-5085, 1986

A:Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteogly A: Reference number: A25442; MUID:86259736

A:Reference number: A25442

A:Residues: 1693-1795, (G, 1797-1855, 1894-2109 <SAI>
A:Residues: 1693-1795, (G, 1797-1855, 1894-2109 <SAI>
A:Residues: 1693-1795, (G, 1797-1855, 1894-2109 <SAI>
A:Cross-references: GE:M13993; NID:9211654; PIDN:AA48720.1; PID:9211655

A:Residues: 1633-1795, (G, 1797-1855, 1898)

A:Residues: 1693-1795, (G, 1797-1855, 1898)

A:Reference number: A32002; MUID:89008500
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A; Residues: 998-1015, X', 1017-1019, 'X', 1021-1023 < KR2>
A; Note: amino end of 86K core peptide CS-A
A; Accession: B37072
A; Molecule type: protein
A; Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 < KR3>
A; Molecule type: protein
A; Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 < KR3>
A; Note: amino end of 75K core peptide CS-B
C; Superfamily: aggrecan; C-type lectin homology; complement; Siewyords: alternative splicing
C; Keywords: alternative splicing
C; Keywords: alternative splicing
C; Fy-20/Domain: signal sequence #status predicted <ART>
F; 1-20/Domain: signal sequence #status predicted <ART>
F; 4-131/Domain: animunoglobulin homology <IMMI>
F; 264-346/Domain: link protein repeat homology <INR2>
F; 537-64/Domain: link protein repeat homology <INR3>
F; 537-64/Domain: link protein repeat homology <INR3>
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ilarity 23.4%;
Conservative 31
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QVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGL 223 

591

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-----SGNLLQVLMSFPSLTNFL 186

368 GSAFTIOTVTOTEVELPLPRNVTEEEARGSIATLEPMEITATATELYEAFTVLPDL--FA 425

163 GDGFSY-----

q ŏ g 4;

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C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 28-Dec-1987 #text_change 22-Jun-1999
C; Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
C; Accession: A28801; A38097; B39097
R; Kiss, I.; Deak, F.; Mestric, S.; Delius, H.; Soos, J.; Dekany, K.; Argraves, W.S.; Proc. Natl. Acad. Sci. U.S.A. 84, 6399-6403, 1987
A; Title: Caracture of the chicken link protein gene: exons correlate with the protein A; Reference number: A28305; MUID:87317659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Accession: 542938
A. Molecule type: mRNA
C. Molecule type: mRNA
C. Molecule type: mRNA
F. 15 Molecule type: matrix; glycoprotein
F. 15 Molecule type: mrnunoglobulin homology < LMNA
F. 176 - 253 Momain: link protein repeat homology < LMNA
F. 274 - 350 Momain: link protein repeat homology < LNNA
F. 274 - 350 Momain: link protein repeat homology < LNNA
F. 274 - 350 Momain: link protein repeat homology < LNNA
F. 274 - 350 Momain: link protein repeat homology < LNNA
F. 274 - 350 Momain: link protein repeat homology < LNNA
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F. 274 - 350 Momain: link protein repeat homology < LNNA
F. 274 - 350 Momain: link protein link protein link protein link prot
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;115-193,235-306,259-280,333-403,358-379/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: cartilage link protein
C;Species: Eguus caballus (domestic horse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EDDTAVVALELOGV---VFPYFPRL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                                                  Length 408;
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                                                                                                                                                                                  DB 1;
                                                                                                                                                                             9.1%; Score 169.5; DB 1
30.8%; Pred. No. 6.4e-07;
iive 20; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: 542938
R; Dudhla, J; Platt, D.
Nomitted to the EMBL Data Library, March 1994
A; Reference number: 542938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 GONTVPGVRNYGFWDKDKSRYDVFCF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
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Best Local Similarity
Matches 45; Conserv
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A; Residues: 1408 < RHO>
R; Doege, K; Hassell, J.R.; Caterson, B.; Yamada, Y.
R; Doege, K; Hassell, J.R.; Caterson, B.; Yamada, Y.
R; Doege, K; Hassell, J.R.; Caterson, B.; Yamada, Y.
P; Doege, K; Hassell, J.R.; Bakell, J.R.; J966
A; Title: Link protein CDNA sequence reveals a tandemly repeated protein structure.
A; Reference number: A24880; MUID:86233314
A; Residues: 180-408 CDOE.
B; Neame, P.J.; Christner, J.E.; Baker, J.R.
A; Residues: 180-408 CDOE.
B; Neame, D.J.; Christner, J.E.; Baker, J.R.
A; Residues: 180-408 CDOE.
B; Neame, D.J.; Christner, J.E.; Baker, J.R.
A; Residues: 180-408 CDOE.
B; Neame, D.J.; Christner, J.E.; Baker, J.R.
A; Residues: 180-408 CDOE.
B; Neame, D.J.; Christner, J.E.; Day Commer: A02869; MUID:86140139
A; Residues: 16-33, A', 89-375, WV, 377-408 CNEA>
A; Residues: 16-33, A', 89-375, WV, 377-408 CNEA>
C; Comment: This protein was extracted from rat chondrosarcoma
C; Comment: Residues 259-277 and 358-376 (approximately) form epitopes for the species-nc
C; Comment: Link protein unink protein; immunoglobulin homology; link protein repeat H
C; Keywords: cartilage; chondroitin sulfate proteoglycan; duplication; glycoprotein; hyal
C; Keywords: cartilage; chondroitin homology CIMA>
F; 16-408/Product: proteoglycan link protein 2 #status experimental CMAT>
F; 230-307/Domain: link protein repeat homology CIMA>
F; 230-307/Domain: link protein repeat homology CIMA>
F; 328-404/Domain: link protein repeat homology CIMA>
F; 328-404/Domain: link protein repeat homology CLNX>
                                                                                                                                                               C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42630
R;Hering, T.M.; Kollar, J.; Huynh, T.D.
Submitted to the EMBL Data Library, September 1996
A;Description: Complete coding sequence of bovine aggrecan: comparative structural analy
A;Reference number: 22182
A;Recession: T42630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mcclaile type: mRNA
A;Residues: 1-2327 KHER>
A;Accession: T42637
A;Residues: 1-2327 KHER>
A;Residues: 1-2327 KHER>
A;Residues: 1-2327 KHER>
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot
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WiAlternate names: cartilage link protein

C;Species: Rattus norvegicus (Norway rat)

C;Decies: Rattus norvegicus (Norway rat)

C;Date: 13-Aug-1986 #sequence_revision 24-oct-1997 #text_change 13-Nov-1998

C;Accession: A28654; A24880; A02869

R;Rhodes, C;;Dooge, K; Ssasali, M; Yamada, Y.

J. Biol. Chem. 263, 6063-6067, 1988

A;Title: Alternative splicing generates two different mRNA sepcies for rat link protein.

A;Reference number: A28654; MUID:88198139

A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%; Score 170; DB 2;
38.9%; Pred. No. 5e-06;
iive 12; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCY 148
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Best Local Similarity 38.9%
Matches 37; Conservative
                                                                                                                                       aggrecan - bovine
                                                                                      T42630
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A;Cross-references: GB:L07049; NID:q678541; PIDN:AAC37670.1; FID:q191772
R;Watanabe, H.; Gao, L.; Suqiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A;Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene struc
A;Reference number: S55329; MUID:95289972
A;Reference number: S55329; MUID:95289972
A;Retaus: preliminary
A;Rolecule type: mRNA
A;Residues: 1-567, (°, 569-1728, 'I', 1730-2132 <WATI>
A;Cross-references: GB:U22901; NID:9686014
A;Cross-references: GB:U22901; NID:9686014
A;Reference number: S50206; MUID:95035091
A;Reference number: S50206; MUID:95035091
A;Reference number: S50206; MUID:95035091
A;Reference number: S50206; MUID:95035091
A;Reference number: S51355
A;Reference number: S51
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A) Introns: 253/1
C) Superfamily: agreean; C-type lectin homology; complement factor H repeat homology;
C) Superfamily: agreean; C-type lectin matrix
C) Superfamily: agreean; C-type lectin matrix
F):1-19/Domain: signal sequence #status predicted <SIG>F):4-13/Domain: immunoglobulin homology <IMM>F):170-24/Domain: link protein repeat homology <ILNK1>F):268-349/Domain: link protein repeat homology <ILNK2>F):504-581/Domain: link protein repeat homology <ILNK2>F):504-581/Domain: link protein repeat homology <ILNK3>F):302-2042/Domain: C-type lectin homology <ILNK4>F):302-2042/Domain: C-type lectin homology <ILNK5>F):204-2105/Domain: complement factor H repeat homology <INK4>F):2049-2105/Domain: complement factor H repeat homology <INK4
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A;Reference number: I58123; WUID:95004579
A;Accession: I78532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Rosidues: 211-240, MCTASLRRWRVRSFWRHPORNSPSRROPTS','AGGWGHAWPPOASSTWPGRAVWTCAALAGW'
A;Cross-references: GB:873720; NID:9765211; PIDN:AAB32159.1; PID:9765212
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: 178532
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Nolecule type: DNA
A;Residues: 211-326 <WATU>
A;Coss-references: GB:S73722; NID:9765215; PIDN:AAB32160.1; PID:9765216
A;Accession: 158123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 OVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%; Score 165; DB 1; 28.8%; Pred. No. 1.2e-05;
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Best Local Similarity 28.8
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-355 < CDEA>
A; Cross-references: GB: M13212; NID: 9212259; PIDN: AAA48940.1; PID: 9212260
A; Cross-references: GB: M13212; NID: 9212259; PIDN: AAA48940.1; PID: 9212260
A; Experimental source: embryonic sternal cartilage
B; Wu, L.N.Y.; Genge, B.R.; Wuthler, R.E.
J. Biol. Chem. 266, 1187-1194, 1991
A; Title: Association between proteoglycans and matrix vesicles in the extracellular matrix A; Reference number: A39097; MUID: 91093230
A; Accession: A39097
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C;Species: Mus musculms (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A55182; S55329; S50207; S51355; I78532; I58123
R;Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, K.J.
Genomics 22, 364-371, 1994
A;Title: Complete coding sequence, deduced primary structure, chromosomal localization, A;Reference number: A55182
A;Accession: A55182
A;A
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A; Residues: 40-55, X', 57-59 <WU2>
A; Note: 39K protein, a minor component of matrix vesicles
C; Comment: Link proteins stabilize the aggregates of proteoglycan monomers with hyaluron
tructures that induce mineralization).
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C; Superfamily: proteglycan link protein; immunoglobulin homology; link protein repeat D
C; Superfamily: proteglycan link protein; extracellular matrix; glycoprotein
C; Keywords: cartilage; duplication; extracellular matrix; glycoprotein
F; 1-15/Domain: signal sequence % status predicted < SIG>
F; 1-15/Domain: signal sequence % status predicted < MAT>
F; 17-25/Product: link protein % status predicted < MAT>
F; 17-25/Domain: immunoglobulin homology < LMXL>
F; 177-25/Domain: link protein repeat homology < LMXL>
F; 27-35/LOmmin: link protein repeat link protein repeat link protein repeat link protein link protein
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R;Deak, F.; Kiss, I.; Sparks, K.J.; Argraves, W.S.; Hampikian, G.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 83, 3766-3770, 1986
A;Title: Complete amino acid sequence of chicken cartilage link protein deduced from A;Reference number: A24881; MUID:86233315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 40-55, X',57-60, X',62-75, X',77-78, X' <WUA>
A;Note: 38K protein, a major component of matrix vesicles; Asn-56 appears to be
A;Accession: B39097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSP- 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | |: :|| GGKNTVPGVRNYGFWDKERSRYDVFCF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-355 <KIS>
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a ò g

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RESULT

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protecylycan link protein precursor - pig
Nalternate names: Cartilage link protein
C:Species: Sus scrota domestica (domestic pig)
C:Species: Sus scrota domestica (domestic pig)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 22-Jun-1999
C:Accession: 804243: I47145
N. Poudhia. J.; Hardingham, T.E.
J. Mol. Biol. 206, 749-753, 1989
A;Title: Appendix. Isolation and sequence of cDNA clones for pig and human cartilage
A;Reference number: 804243
A;Reference number: 804243
A;References: ENBL:Y00165; NID:g2009; PIDN:CAA68358.1; PID:g2010
A;Cross-references: EMBL:Y00165; NID:g2009; PIDN:CAA68358.1; PID:g2010
A;Title: Immunoglobulin fold and tandem repeat structures in protecylycan N-terminal
A;Reference number: 147145
A;Strus: preliminary; translated from GB/EMBL/DDBJ
A;Reference number: 147145
A;Strus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-354 cPRE>
A;Strus: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:Y00165; NID:g2009; PIDN:CAA68358.1; PID:g2010
C;Superfamily: protecylycan link protein; immunoglobulin homology clums
C;Keywords: cartilage: duplication: extracellular matrix: glycoprotein
C;Superfamily: protecylycan link protein #status predicted cMAT>
F;16-354/Product: protecylycan link protein #status predicted cMAT>
F;16-354/Product: protecylycan link protein #status predicted
F;141/Domain: ilink protein repeat homology cLUM3
F;145-230-Domain: ilink protein repeat homology cLUM3
F;145-350-Domain: ilink protein repeat homology cLUM3
F;145-350-Domain: ilink protein repeat homology cLUM3
F;145-350-Domain: ilink protein repeat homology cLUM3
F;145-130-Domain: ilink protein repeat homology cLUM3
F;145-130-Domain: ilink protein repeat homology cLUM3
F;145-130-Domain: ilink protein repeat homology cLUM3
F;145-130-Dumain: ilink protein repeat homology cLUM3
F;145-130-Dumain: ilink protein repeat homology cLUM3
F
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aggrecan precursor - human
MyAlternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jan-2000
C;Accession: A39086; S50206; A43919; S46659; S66389; S68646; B43919; C43919
R;Doege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
                                         GOYKLTFDKAREACANEAATMATYNQLSYXOKAKYHLCSAGWLETGRVAYPTAFASONCG 124
                                                                                                                                                                                 135 GRYKCE----VIEGL-----VIFFRL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
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5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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Best Local Similarity 29.5%; Pred. No. 2.6e-06;
Matches 43; Conservative 22; Mismatches 52
                                                                                                                                                                                                                                                                                   125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                   228 GONTVPGVRNYGFWDKDKSRYDVFCF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
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   NATEGRAPH OF A DESCRIPTION OF A DESCRIPT
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30.1%; Pred. No. 1.7e-06;
tive 21; Mismatches 52;
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Matches 44; Conservative
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4

Gaps

29;

Indels

us-09-466-778-11.rpr

Length 2316;

DB 1;

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8.7%; Score 161.5; DB 1
27.9%; Pred. No. 2.7e-05;
iive 22; Mismatches 64
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Job time: 44 sec
                                                                                                    Best Local Similarity 27.93
Matches 50; Conservative
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Best Local Similarity
Matches 34; Conserv
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A; Molecule type: protein
A; Genetics:
C; Genet
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A; Residues: 764-765, A, 767-846, VV, 848-862, Xx, 864 <BAR>
A; Residues: 764-765, A, 767-846, VV, 848-862, Xx, 864 <BAR>
A; Recors-references: EMBL:S74659; NID:9807127; PIDN:AAC60643.1; PID:9807128
A; Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue
A; Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue
Arch. Blochen. Blochen. 22-30, 1995
A; Title: Catabolism of aggreean by explant cultures of human articular cartilage in the
A; Reference number: S66389; MUID:96004775
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J. Biol. Chem. 266, 894-902, 1991
A;Title: Complete coding sequence and deduced primary structure of the human cartilage
A;Reference number: A39086; MUID:91093289
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A,Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the
                                                                                                                                                                                                                                                                                                                                                                                     R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues
A;Reference number: S50206; WID:95035091
A;Accession: S50206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 350-497 <GLU>
A,Cross-references: EMBL:X80278; NID:9516295
A,Koross-references: Embl.x80278; NID:9516295
A,Note: this translation is not annotated in GenBank entry HSAGGREC, release 113.0
R,Sandy, J.D.; Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
J. Clin. Invest. 89, 1512-1516, 1992
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A; Residues: 361-370, X', 372-373:393-399, 'X', 401-407, 'X', 409 <SAN>
A; Residues: 361-370, X', 372-373:393-399, 'X', 401-407, 'X', 409 <SAN>
A; Experimental source: synovial fluid
A; Note: sequence modified after extraction from NCBI backbone
B; Barry, F.P: Neame, P.J:; Sasse, J:; Pearson, D.
Matrix Biol. 14, 323-328, 1994
A; Title: Length variation in the keratan sulfate domain of mammalian aggrecan.
A; Reference number: 146998; MUID:95128522
A; Accession: S46659
                                                                                                                                                                                                                                                                                          A;Residues: 1.2316 <DOE>
A;Cross-references: GB:M55172; NID:g178258; PIDN:AAA62824.1; PID:g178259
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A;Accession: S68646
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A;Residues: 17-23;24,'X',26-27;393-401;402-403 <LLI>
R;Fosang, A.J; Last, K; Knaeuper, V.; Murphy, G.; N
FEBS Lett. 380, 17-20, 1996
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A; Status: preliminary
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                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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A; Molecule type: protein
A; Residues: 1-28, 'T', 30-370 <BAR1>
R; Barry, F.P.; Gaw, J.U.; Young, C.N.; Neame, P.J.
Bochem. J. 291, 951, 1993
A; Title: Correction. Hyaluronan-binding region of aggrecan from pig laryngeal cartila
A; Reference number: S32530; MUID: 93256913
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A;Residues: 25-55 CABRA2>
A;Note: correction to sequence S29139
R;Fosang, A.J.; Neame, P.J.; Last, K.; Hardingham, T.E.; Murphy, G.; Hamilton, J.A.
J. Bhlo.; Chem. 267, 19470-19474, 1992
A;Title: The interglobular domain of cartilage aggrecan is cleaved by PUMP, gelatinas
A;Reference number: A44108; MUID:92406898
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A;Residues: 345-348, NF', 349-351 <FOS>
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology;
C;Reywords: cartilage; chondroith sulfate proteoglycan; extracellular matrix; glycop
F;28-119/Domain: immunoglobulin homology <IMM>
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F;252-333/Domain: link protein repeat homology <LNK2>
F;252-333/Domain: link protein repeat homology <LNK2-
F;10,223;317/Binding site: carbohdrate (Asn) (covalent) #status experimental
F;355,360/Binding site: keratan sulfate (Thr) (covalent) #status experimental
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Bate: 30-Sep-1993 #sequence_revision 18-Mar-1997 #text_change 13-Aug-1999
C;Accession: S29139; S32530; A44108
R;Barry, F.P.; Gaw, J.U.; Young, C.N.; Neame, P.J.
Biochem, J. 286, 761-769, 1992
A;Title: Hyaluronan-binding region of aggrecan from pig laryngeal cartilage.
A;Reference number: S29139; MUID:93038505
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                                                                                                                                                ---VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKA
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35.8%; Pred. No. 3.7e-06;
tive 16; Mismatches 41;
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Sequence 7, Appli
Sequence 3, Appli
Sequence 2, Appli
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Sequence 7, Appli
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Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08024868
Patent No. 5386013
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine_Induced Protein, TSG-6, DNA
TITLE OF INVENTION: Cytokine_Induced Protein, TSG-6, DNA
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.1%; Score 262; DB 1; L
Best Local Similarity 43.3%; Pred. No. 8e-21;
Matches 45; Conservative 16; Mismatches 43;
US-08-483-322-7
US-08-478-882-7
US-08-92-882-7
US-07-946-497-2
US-09-191-647-7
US-09-191-647-7
PCT-US91-09055-2
US-08-192-855-8
US-08-872-855-8
US-08-872-855-7
US-08-872-855-7
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US-08-872-855-4
US-08-872-855-4
US-08-107-159-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/024,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/642,312
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, NW
CITY: Washington
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NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: VI
TELECOMMUNICATION INFORMATION:
TELEPANE: 212-628-5197
TELEFAX: 212-737-3528
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  363
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US-08-024-868-2
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Sequence 3, Appli
Sequence 9, Appli
                                                                                             4, 2001, 13:03:56 ; Search time 13.89 Seconds
   (without alignments)
   456.360 Million cell updates/sec
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Sequence 6, A
Sequence 6, A
Sequence 4, A
Sequence 8, A
Sequence 8, A
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Sequence 2, 8
Sequence 34, 8
Sequence 34, 8
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Sequence 2,
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
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Compugen Ltd
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US-08-225-097-2

US-08-225-1795-1

US-08-225-0475-6

US-08-225-0473-8

US-08-225-0473-8

US-08-225-0473-8

US-08-225-0473-3

US-08-225-0473-3

US-08-225-0473-3

US-08-225-0473-3

US-08-225-0473-4

PCT-US95-0435-3

US-08-225-0477-2

US-08-225-0477-2

US-08-225-0478-3

US-09-273-565-34

US-09-273-565-34

US-09-273-565-34

US-09-273-565-34

US-09-273-565-34

US-09-273-565-34

US-09-273-565-34
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               GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                   - protein search, using
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Maximum DB seq length: 200000000
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1857
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99
98.5
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52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
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GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: BLABB, A Brain Hya-
TITLE OF INVENTION: Longe Steward Johnston & Reens
STREET: 986 Bedford Street
CITY: Stamford
STATE: CT
COUNTRY: United State
                                                          STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 43.3%; Pred. No. 8e-2
Matches 45; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           WISNIEMSKI-1
                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,311
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPPRATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/225,477B
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                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: 212-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Processor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: April 8, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 277 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mary M. Krinsky
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                                                                                                                                                                                                                                          FILING DATE
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Protein for Treating Inflammatory Diseases and Cancer-Related
Methods of Using same
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    Sequence 2, Application US/08242097
Patent No. 5846763
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Wilcek, Hans Georg
APPLICANT: Wilcek, Hans Georg
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                     112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.1%; Score 262; DB 2;
43.3%; Pred. No. 8e-21;
tive 16; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEEZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-73/-33.0
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 277 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-242-097-2
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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PCT-US96-11995-1
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65 GQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wishiewski, Hans Georg
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Wishiewski, Hans Georg
TITLE OF INVENTION: Therefor and Uses Thereof
TITLE OF INVENTION: Therefor and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.0%; Score 167; DB 4; Length 326; Best Local Similarity 31.5%; Pred. No. 3.2e-10; Matches 46; Conservative 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEACHIN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Doege, K., Hassell, J.R., Ca-AUTHORS: terson, B., and Yamada, Y.
TITLE: Link protein cDNA sequence reveals a
JUILE: tandemly repeated protein sequence.
JOURNAL: Proc. Natl. Acad. Sci. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
                                               1751-P0004
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                                                                                                                                                                                                                                                                                             polypeptide
functional domains
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; Sequence 4, Application US/08242097
; Patent No. 5846763
; GENERAL INFORMATION:
                                      REFERENCE/DOCKET NUMBER: 1751
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEPAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 residues
TYPE: amino acid
STRANDEDNESS: single
  NAME: Mary M. Krinsky REGISTRATION NUMBER: 32423
                                                                                                                                                                                                                                                                                                                                                                rat link protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 3761-3765
DATE: 1986
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STATE: D.C.
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DESCRIPTION:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score 167; DB 1; Length 326; 31.5%; Pred. No. 3.2e-10; Live 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: 1uronan-Binding Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: 5t. Onge Steward Johnston & Reens
STREET: 986 Bedford Street
CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Doege, K., Hassell, J.R., Ca-AUTHORS: terson, B., and Yamada, Y.
TITLE: Link protein cDNA sequence reveals of TITLE: tandemly repeated protein sequence. JOURNAL: Proc. Natl. Acad. Sci. USA
REGISTRATION NUMBER: 32423
REFERENCE/POCKET UMBER: 1751-P0004
TELECOMMUNICATION:
TELEPHONE: 203-324-6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GQNTVPGVRNYG-FWDKDSRYDVFCF 226
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functional domains
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APPLICATION WHERE:
FILING DATE: April 8, 1994
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: rat link protein PUBLICATION INFORMATION:
                                                                                   TELEFAX: 203-227-1096
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 326 residues
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CT
COUNTRY: United States
2TP: 06905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.09
Best Local Similarity 31.59
Matches 46; Conservative
                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 3761-3765
DATE: 1986
                                                                                                                                                                                                                                                                   DESCRIPTION:
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
PCT-US95-04353-6
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256 -----GELFLGAPPG--KLTWEEARDYCLERGAQIASTGQLYAAWNGGLDRCSPGWLADG 308
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                                                                                                                                                                                                                                                                                     51 QDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETG 110
                                                                                                                                                                                                 10 ECKSHYVGDGLNCEPEQLPIDRCLQD-------NGQCHADAKCVDLHF 50
                                                                                                                                                       37;
                                                                                                               Length 371;
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                                                                                                        8.5%; Score 157.5; DB 1; Length 3' nilarity 27.9%; Pred. No. 4.3e-09; Conservative 22; Mismatches 60; Indels
  polypeptide encoded by (and set out under) SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: rat BEHAB
OTHER INFORMATION: polypeptide encod-
OTHER INFORMATION: ed by (and set out under) SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                111 RVAYPTAFASQNCGSGVVGIVDYGPRPN-----KSEMWDVFCYR 149
                                                                                                                                                                                                                                                                                                                                                                                                     309 SVRYPIITPSQRCGGGLPGVKTLFLFPNQTGFPSKQNRFNVXCFR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREE: St. Onge Steward Johnston & Reens STREET: 986 Bedford Street CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,477
FILING DATE: APril 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
DESCRIPTION: polypeptide
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. NO: ... 371 amino acids ... 371 amino acids STRANDEDNESS: sirr TOPOLOGY: 1: ... OUBCULF ...
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FIELERAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States ZIP: 06905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-225-477B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
                                                                                                               Query Match
Best Local Similarity
Matches 46; Conservi
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PCT-US95-04353-8
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                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08225477B

Patent No. 5635370

GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: Luronan-Binding Protein
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge Steward Johnston & Reens
STREET: 986 Bedford Street
    NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE26/VILCEK-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AFASQNCG--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 TKPREPCGGQNTVPGVRNYGFWDKDKSRYDVFCF 96
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225.477B
FILING DATE: APril 8, 1994
ATTORNEY/AGENT INFORMATION:
NAME: MALY M. Krinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1751-P0004
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REGISTRATION NUMBER: 32423
REGISTRATION NUMBER: 1751
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAX: 203-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: polypeptide
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: rat brain
                                                                                                             TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 anino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: rat BEHAB
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MOLECULE TYPE:
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STATE: CT
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51 QDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETG 110
                          107 LETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GKHKCECKSHYVGDGLNCEPEQLPIDRC------LQDNGQCHADAKCVDLHF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 157; DB 1; Length 329; 26.8%; Pred. No. 4.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Doege, K., Sasaki, M., Hori-AUTHORS: gan, E., Hassell, J.K., and Yamada, Y.
TITLE: Complete primary structure of the rat
TITLE: cartilage proteoglycan core protein deduced from
                                                                                                                                                                                                                                                                                                                                         E: St. Onge Steward Johnston & Reens
986 Bedford Street
                                                                                                                                         Sequence 3, Application US/08225477B
Patent No. 5635370
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.1e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/225,477B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               functional domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMUNICATION INFORMATION:
TELECOMUNICATION: 203-324-6155
TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/
FILING DATE: April 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Processor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE: cDNA clones.
JOURNAL: J. Biol. Chem.
VOLUME: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: rat aggrecan
                                                                                                                                                                                                                                                                                                                                                                                                                               United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 26.8
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 17757-17767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: Sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 STREET: 986 Bec
CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06905
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                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                        RESULT 10
US-08-225-477B-3
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                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                               47 DLHFQDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGW 106
                                                                                                                                                                      51 QDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETG 110
                                              Gaps
                                                                                    ----NGQCHADAKCVDLHF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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    Length 371;
                                          Indels
                                                                                                                                                                                                                                                         111 RVAYPTAFASQNCGSGVVGIVDYGPRPN-----KSEMWDVFCYR 149
                                                                                                                                                                                                                                                                                   | | | | : | : | : | : | 309 SVRYPIITPSQRCGGLPGVKTLFLFPNQTGFPSKQNRFNVYCFR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/340,428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8e-08;
rhes 53;
8.5%; Score 157.5; DB 4; 27.9%; Pred, No. 4.3e-09; tive 22; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.5%; Score 157.5; Best Local Similarity 34.2%; Pred. No. 2.8e Matches 41; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Margolis=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49, Application US/08340428B Patent No. 5648465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGIETRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Marg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                    10 ECKSHYVGDGLNCEPEQLPIDRCLQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
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                                            46; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
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ADDRESSEE: Browdy an
                 Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Sever CITY: Washington STATE: D.C.
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47 DLHFQDTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGW 106
228 AEEMEGEFYATSP---EKFTFQEAANECRTVGARLATTGQLYLAWQGGMDMCSAGWLADR 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: R.K.
TITLE: Cloning and primary structure of neu-
TITLE: rocan, a developmentally regulated, aggregating
TITLE: chondroitin sulfate proteoglycan of brain.
JOHNANL: J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 LETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCY 148
                                          111 RVAYPTAFASQNCGSGVVGI-----VDYGPRPNKSEMWDVFCY 148
                                                                         285 SVRYPISKARPNCGGNLLGVRTVYLHANQTGYPDPSSRYDAICY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Rauch, U., Karthikeyan, L.,
AUTHORS: Maurel, P., Margolis, R.U., and Margolis,
                                                                                                                                                                                                                                                                                                                                                                              E: St. Onge Steward Johnston & Reens
986 Bedford Street
                                                                                                                                                                                                                                              APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,477B
FILING DATE: April 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
functional domains
                                                                                                                                                                                    Sequence 4, Application US/08225477B Patent No. 5635370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION
TELEPHONE: 203-324-6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 203-324-6155
TELEPAX: 203-327-1096
INFORMATION FOR SEQ ID NO: ...
SEQUIENCE CHARACTERISTICS:
LENGTH: 333 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: rat neurocan PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 06905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mary M. Krinsky REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES: 19536-19547
DATE: 1992
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Matches 37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
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CITY: Stamford
STATE: ۲۳
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DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 157; DB 4; Length 329;
; Pred. No. 4.1e-09;
23; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Doege, K., Sasaki, M., Hori-
AUTHORS: gan, E., Hassell, J.R., and Yamada, Y.
TITLE: Complete printry structure of the rat
TITLE: cartilage proteoglycan core protein deduced from
TITLE: cDNA clones.
JOURNAL: J. Biol. Chem.
                             285 SVRYPISKARPNCGGNLLGVRTVYLHANQTGYPDPSSRYDAICY 328
  111 RVAYPTAFASQNCGSGVVGI-----VDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                  ADDRESSEE: St. Onge Steward Johnston & Reens STREET: 986 Bedford Street STREET: Stamford STREET
                                                                                                                                            Sequence 3, Application PC/TUS9504353
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: Inronan-Binding Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 157;
26.8%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
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functional domains
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APPLICATION NUMBER: 08/225,477
FILING DATE: APril 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MATY M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAX: 203-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TRNGTH: 329 residues
                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: rat aggrecan PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGES: 17757-17767
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Best Local Similarity
Matches 44; Conserve
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            06905
                                                                                                           RESULT 11
PCT-US95-04353-3
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202 QCDAGWLSDQTVRYPIQTPREACYGDMDGFPGVRNYGVVDPD----DLYDVYCYAEFLNG 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ECKSHYVGDGLNCEPEQLPIDRC-----LQDNGQCHADAKCVDLH----FQDTTVG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08242097
Patent No. 5846763
GENERAL INFORMATION:
APPLICANT: Lea Ho
APPLICANT: Visioniewski, Hans Georg
APPLICANT: Visioniewski, Hans Georg
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF EQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 912;
                                                                                                Sequence 2, Application PC/TUS9503747
GENERAL INFORMATION:
APPLICANT: LA JOLIA CANCER RESEARCH FOUNDATION
TITLE OF INFORTION: Brevican, A Glial Cell Proteoglycan
NUMBER OF SEQUENCES: 3
186 LSDRIVRYPITQSRPGCYGDRSSLPGVRSYG-RRDPQELYDVYCF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
                                                                                                                                                                                                                                          E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AFASONCGSGVVGI-----VDYGPRPNKSEMWDVFCYR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 VTPSQRCGGGLPGVKTLFLFPNQTGFPNKHSRFNVYCFR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8,4%; Score 155.5; DB 4
28.3%; Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-MRR-1995
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 97,643
REGISTRATION NUMBER: FP-LJ 1453
RELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL STREET STRESS TO TYPE: amino acid TOPOLOGY: li-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: protein
PCT-US95-03747-2
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSE: Campbell
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                    STREET: 4370 La JC
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                               COUNTRY: U
                                                                    RESULT 14
PCT-US95-03747-2
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US-08-242-097-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.4%; Score 156; DB 4; Length 333; Best Local Similarity 35.2%; Pred. No. 5.4e-09; Matches 37; Conservative 18; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE: Cloning and primary structure of neu-
TITLE: rocan, a developmentally regulated, aggregating
TITLE: chondroitin sulfate proteoglycan of brain.
JOURNAL: J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCY 148
  186 LSDRTVRYPITQSRPGCYGDRSSLPGVRSYG-RRDPQELYDVYCF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Rauch, U., Karthikeyan, L., AUTHORS: Maurel, P., Margolis, R.U., and Margolis,
                                                                                                                                                                                                                                                                                                            E: St. Onge Steward Johnston & Reens 986 Bedford Street
                                                                                                                               Sequence 4, Application PC/TUS9504353
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: 1 Uronan-Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET UNMBER: 1751-P0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEPHONE: 203-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC '
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,477
FILING DATE: APril 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide
functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: rat neurocan PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1(
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19536-19547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   STREET: 986 Bed
CITY: Stamford
STATE: CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UN
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                                                                                         RESULT 13
PCT-US95-04353-4
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CITY: Washington

STATE: D. D. C. GONDUTER READABLE FORM:

STATE: D. 20004

COMPUTER READABLE FORM:

MEDIONY TYPE: Floppy disk

COMPUTER: INP Compatible

SOFTWARE: D. PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

ATTORNEY/AGBNT INFORMATION:

NAME: BRENGONY ROGER IN-1994

ATTORNEY/AGBNT INFORMATION:

RECERCANION INFORMATION:

RECERCANION INFORMATION:

RECERCANION INFORMATION:

RECERCANION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 97 annino acids

STRANDENESS: single

STRANDENESS: Sin
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Search completed: April 4, 2001, 13:04:18 Job time: 22 sec

Wed Apr 4 13:03:52 2001

## SEQ 1D11, Database; SPTREMBL-15 Fle Copy SEQ 1D11, Darabask, -... us-09-466-778-11. rspt AC NOS.: Q9NRY3, Q9UF98

Page 1

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

April 4, 2001, 13:04:01; Search time 27.49 Seconds (without alignments) 1505.071 Million cell updates/sec Run on:

US-09-466-778-11 1857 Title: Perfect score: Sequence:

1 MTGPGKHKCECKSHYVGDGL.....ALAAYSYFRINRKTIGFXHF 353

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

374700 seqs, 117207915 residues Searched:

Total number of hits satisfying chosen parameters:

374700

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\* SPTREMBL\_15:\*
1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fung1:\*
4: sp\_human:\* sp\_organelle:\* sp\_plant:\* sp\_rodent:\* sp\_phage: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
		ф					
Result		Query					
No.	Score	Match	Match Length DB	DB	ឧ	•	Description
-	1757	94.6	897	4	Q9NRY	3	O9nry3 homo sapien
7	1468	79.1	1069	4	Q9UF98	8	homo
e	662	35.6	2212	4	093072	2	homod
4	645.5	34.8	2570	4	1 W 60	2	Q9ny15 homo sapien
'n	264	14.2	275	11	0088	59	008859 mus musculu
9	177	9.5	2109	13	P797	87	P79787 gallus gall
7	169.5	9.1	355	11	09Z1	X7	Q9z1x7 mus musculu
80	162	8.7	1321	4	01459	4	014594 homo sapien
6	161.5	8.7	655	11	0885	64	O88564 rattus norv
10	161.5	8.7	1290	13	9M60	E1	O9w6el qallus qall
11	160.5	8.6	2394	9	07761	0	077610 bos taurus
12	153	8.2	192	9	00281	7	002817 oryctolagus
13	153	8.2	929	9	07761	7	077612 bos taurus
14	151.5	8.2	1643	9	07761	1	077611 bos taurus
15	151.5	8.3	3381	9	07760	0	077609 bos taurus
16	126.5	9.9	103	9	Q9TTB		Q9ttb3 sus scrofa
17	120.5	6.5	103	9	.04638	0	046380 oryctolagus
18	110	5.9	368	13	Q9W6S4	S4	Q9w6s4 gallus gall
19	109	5.9	302	4	O9UNE		Ogunf4 homo sapien

Q995y7 homo sapien	091bg4 xenopus lae	057462 brachydanio	092493 homo sapien	Oyvity drosophila Oy0509 rattus norv O9uj36 homo sapien O97569 ceratotheri O91902 xenopus lae O24530 vitis vinif P79754 fugu rubrip O98f50 arabidopsis
Q93791 caenorhabdi	070474 rattus norv	060494 homo sapien	016004 lytechinus	
Q23587 caenorhabdi	09ntm2 homo sapien	Q9gyx8 mus musculu	008779 rattus norv	
P87357 brachydanio	090656 gallus gall	Q20204 caenorhabdi	0997f8 drosophila	
4 2 2 E	13 13 13	13	294 4 092493 531 5 016004 780 11 008779 480 5 09V7F8 504 5 09XVV4	
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0.00.0	ຄ. 4. 4. 4.	ឯងលំលំលំ	ເພື່ອພິພິພິເ	
		28 99.5 29 99.5 30 99 31 99		388 399 404 421 421 434 43 444 95.55 95.54 96.54 96.54

## ALIGNMENTS

E 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1. 1. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	SEQUENCE FROM N.A.  Tao Q., Zhang W., Cao X.;  Tao Q., Zhang W., Cao Y.;  Ty Match  Ty	Conservative 3 HKCECKSHYVGDGLNCEP	
1 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 209RY3 209RY3 209RY3 200CT-2000 (TEBMELN 01-OCT-2000 (TEBMELN 02.0CT-2000 (TEBMELN 02.0CT-2000 (TEBMELN 03.0CT-2000 (TEBMELN 03.0CT	SEQUENCE FROM N.A. TAGO Q., Zhang W., "Molecular cloning with CD44.", Submitted (JUN-199 EMBL, AF166476; AA SEQUENCE 897 AA;	331; Conse	RSPLGQYKLTED RSPLGQYKLTED RSPLGQYKLTED SNCGSGWGLVD
	D N	One	Matches  Qy., 1 N  Db 489 M	61 121 609 181 669

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Glycoprotein
                                                                                                              01-FEB-1997
01-0CT-2000
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241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXXVGIVGDGFSYSGNLLQVLMSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VSMFFYNDLVNGTTLOTRLGSKLLITDRODPLHPTETRCVDGRDTLEWDICASNGITHVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  861 CIS-------RTPDDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SLINFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGLGENETLSGRDIEHHLAN
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 SRXLKAPPAPVTLXHTXLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
                                                                         301 SRXLKAPPAPVTLXHTXLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann Spünfited (NOY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; All 33021; CAB61358.1; -- HSSP; P98066; ITSG.
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1069 AA; 115666 MW; 04B0950932164D63 CRC64;
                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 115.7 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.1%; Score 1468; DB 4;
80.5%; Pred. No. 1.2e-133;
11ve 4; Mismatches 29;
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                                                                                                                                                                                                                PRT; 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPRO00538; .
INTERPRO; IPR000561; .
INTERPRO; IPR000561; .
INTERPRO; IPR000561; .
INTERPRO; IPR000069; .
INTERPRO; IPR000049; .
INTERPRO; IPR001049; .
INTERPRO; IPR001186; .
INTERPRO; IPR01186; .
INTERPRO; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.1
Best Local Similarity 80.5
Matches 284; Conservative
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                   DKFZP434E0321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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090F98;
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1916 ADGGNGRVGIVSLGARKNLSERMDAYCFRVQDVACRCRNGFVGDGISYCNGKLLDVLAAT 1975
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EMBL; D84433; BAA13377,; -. HSSP; P98066; ITSG.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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9e-55;
158; Indels
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Last sequence update)
Last annotation update)
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2212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 662; D 40.2%; Pred. No. 4 9 rative 47; Mismatches
                                                                                                                   MYELOBDAST KIAA0246 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1265; LINKMODDILE. PROSITE; PS00022; EGF_1; UNKNOWN_5. PROSITE; PS00086; CYTOCHROME_P45Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01186; EGF 2; 13.
PROSITE; PS01241; LINK; UNKNOWN_1 PROSITE; PS01248; LAMININ_TYPE_EGF
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237451 MW;
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Best Local Similarity 40.23
Matches 143; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR001128; -. INTERPRO; IPR002049; -. PFAM; PF00008; EGF; 13. PFAM; PF00193; Xlink; 1.
                                                                                                                                                                 ens (Human).
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INTERPRO; IPRO00561;
INTERPRO; IPRO00782;
                                                                                                                                                                                                                                                                                                                 TISSUE-BONE MARROW
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N. A.
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SEQ ID 11, Database: A-geneseg-36 AC NO. W84087 s-09-466-778-11.rag

New TSG-6 compositions to treat inflammatory diseases and cancer can be complexed with inter-alpha-inhibitor, to treat auto-immune disease, cancer-related pathology etc. can also be administered as \$\pi^SG-6 DNA\$

Chaim 2; Page 58-59; 76pp; English.

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The sequence is that of tumour necrosis factor (TNF) induced glycoprotein TSG-6. TSG-6 is induced in connective tissue by TNF and interleukin-7, and interferes with cell adhesion, to ther cells or the extracellular metrix. It and antibodies specific for it are useful in diagnosis (including identifying susceptibility) and treatment of various disorders associated with cytokine (inhactivation e.g. chronic inflammation (esp. whape associated with proteoglycan breakdown, such as Theumatoid arthritis) cancer (esp. development of metastases) and infections (esp. those quused by Gram negative bacteria).
                                                                                                                                                               Tumour neckosis factor-induced (glyco)protein mol. TSG-6 and its antibody - for treatment and diagnosis of chronic inflammatory conditions e/g. rheumatoid arthritis, infections, sepsis and
                                                                            Wisniewski HG;
                                                                                                                                                                                                                                                        122pp; English
         910S-0642312
                                        (UYNY) UNIV NEW YORK STATE
                                                                                                             -284330/34
                                                                            Vilcek J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 AA;
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14-JAN-1991;
                                                                                                                                                                                    antibody - Ko
                                                                                                             WPI; 1992
N-PSDB; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                            Lee TH
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52 DITVGVFHLRSPLGOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111 Gaps : ||:| : |:||||: ||: | | :||| || :||:|||: || 32 eraagyyhrearsgkykltyaeakavc&fegghlatykqleaarkigfhvcaagwmakgr 91 ő Length 277; Indels 112 VAYPTAFASONCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155 Score 262; DB 13; Pred. No. 1.6e-19; Mismatches 43; 14.18; Sc. 43.38; Pre Query Match 14.1 Best Local Similarity 43.3 Matches 45; Conservative ద ö g

Tumour necrosis factor-stimulated gene-6 protein. W13654 standard; protein; 277 AA 07-NOV-1997 (first entry) RESULT W13654 

1SG-6; human; tumour necrosis factor-stimulated gene-6 protein; treat; inflammatory disease; cancer-related pathology; inhibit; metastasis; invasive tumour growth; rheumatoid arthritis; cathexia; atherosclerosis; systemic lupus erythematosus; rational drug design

Homo sapiens

W09704075-A1

19-JUL-1996; 06-FEB-1997

95US-0001311 10-JUL-1995; (UYNY ) UNIV NEW YORK STATE

Cronstein BN, Vilcek J, Wisniewski H;

WPI; 1997#132619/12.

ö This protein is the human tumour necrosis factor-stimulated gene-6 protein (TSG-6). It can be used in a claimed pharmaceutical composition for treating inflammatory diseases and disorders, or cancer-related pathologies. The composition or DNA encoding TSG-6 may be used to inhibit tumour menastases, invasive tumour growth or cancer-related pathologies. They may also be used in the treatment of inflammatory conditions including rhammatoid arthritis, systemic lupus erythematosus, and nseq Gaps. AREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111 32 eraagvyhrearsgkykltyaeakavcefegghlatykqleaarkigfhvcaagwmakgr 91 including rhaumatoid arthitis, systemic lupus erythematosus, and infections such as cachexia, atherosclerosis etc. TSG-6 can also be to design drugs to treat these disorders. ö Length 277; Indels KSEMWDVFCYRMKDVNC 155 43; .1%; Score 262; DB 18; 3%; Pred. No. 1.6e-19; 16; Mismatches 43; 112 VAYPTAFASQNCGSGVVGIVDYGPRP 52 DTTVGVFHLRSPLGQYKLTFD Query Match
Best Local Similarity 43/3
Matches 45; Conservative Sequence g ò 셤

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W84087 standard; Protein; 277
RESULT
           W84087
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W84087;

10-FEB-1999 (first entry)

recombinant; human; disorder; infection; cancer; hepatitis. Tumour necrosis factor stimulated gene 6; TSG-6; diagnosis; cytokine; immune disorder; autoimmune inflammatory disease; neurodegenerative disease;

Tumour necrosis factor stimulated gene 6 (TSG-6) protein.

/note- "putative signal sequence" 20.277 /note- "mature protein" Location/Qualifiers Homo sapiens Peptide Protein 

118..120 /note= "potential Asn-glycosylation site" 258..260 /note= "potential Asn-glycosylation site" Modified-site Modified-site

US5846763-A

94US-0242097 13-MAY-1994; 08-DEC-1998

94US-0242097. 91US-0642312. 93US-0024868. 14-JAN-1991; 01-MAR-1993;

13-MAY-1994;

(UYNY ) UNIV NEW YORK STATE

Lee TH, Vilcek J, Wisniewski

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protein. A prokaryotic host cell transformed, or a eukaryotic host cell transfected with expression vectors containing the TSG-6 nucleic acid are used to produce recombinant human TSG-6 protein. TSG proteins, peptide fragments of TSG proteins or antibodies to TSG proteins are useful for inactivity, such as immune and autoimmune disorders, infections, inflammatory diseases, neurodegenerative diseases, cancer and alcoholinduced hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                           DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zollinger Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's Alsease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotick wound healing; tissue repair.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                            DNA encoding tumour necrosis factor stimulated gene 6 protein - useful for producing recombinant protein for diagnosis and therapy of disease e.g. immune disorders or cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; transmembrane protein; human; enterocolitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid sequence of protein PRO271.
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                                                                                                       Claim 2; Fig 3A-C; 65pp; English
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970S-0059115.
970S-0059117.
970S-0059119.
970S-0059121.
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97US-0059263.
97US-0059266.
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97US-0062285
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Matches 45; Conservative
WPI; 1999-059056/05.
N-PSDB; V71778.
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The CDNA sequences are obtained transmentain number of the CDNA sequences are obtained transmentain number of the CDNA sequences are obtained transmentain number of the CDNA sequences are obtained brain, fetal liner and fetal retina. The condender of polypeptides, e.g. PRO211 and PRO217 can\begin{array}{c} based on their homology to known polypeptides, e.g. PRO211 and PRO217 can\begin{array}{c} based on their homology to known polypeptides, e.g. PRO211 and PRO217 can\begin{array}{c} based on their homology to mucosa and the repair of acute and chronic mucosa lasions and the repair of acute and chronic mucosa lasions associated ulceration and congenital microvillus atrophy), sk\n diseases associated ulceration and congenital microvillus atrophy), sk\n diseases associated ulceration and congenital microvillus atrophy), sk\n diseases associated cancers such as lung squamous cell carcinoma of the \u03b3\n vulva and gliomas), potent effects on cell growth and development, diseases related to growth cancer sucival of nerve cells including parkinson's diseases related to growth cases, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as an anti-thrombotic agent, PRO287 polypeptides and portions may have thrombotic agent, PRO287 polypeptides and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y13344-403 represent secreted and transmembrane human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yuan J;
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                             97us-0063120.
97us-0063121.
97us-0063127.
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970S-0065186.
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970S-0066364.
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SEG 10 11 , Dathbase : A-grassg. 36 1 1 Us-09-466-778-11. rag AL NO. W84087

This protein is the human tumour necrosis factor-stimulated gene-6 protein (TSG-6). It can be used in a claimed pharmaceutical composition for treating fullammatory diseases and disorders, or cancer-related pathologies. The composition or DNA encoding TSG-6 may be used to inhibit tumour metastases, invasive tumour growth or cancer-related pathologies. They may also be been in the treatment of inflammatory conditions including rheumatola arthritis, systemic lupus erythematosus, and infections such as cachesia, atherosclerosis etc. TSG-6 can also be used to design drugs to treat these disorders. 52 DTTVGVFHLRSPLGQYKLTFDKAREACANEÀATMATYNQLSYXOKAKYHLCSAGWLETGR 111 New TSG-6 compositions to treat inflammatory diseases and cancer-den be complexed with inter-alpha-inhibitor, to treat auto-immune diaease, cancer-related pathology etc. can also be administered as TSG-MG DNA Query Match
Best Local Similarity 43.38
Matches 45; Conservative Sequence 셤 The sequence us that of tumour necrosis factor (TNF) induced glycoprotein \$8G-6. TsG-6 is induced in connective tissue by TNF and interleuth-7, and interferes with cell adhesion to ther cells or the extracellular matrix. It and antibodies specific for it are useful in diagnosis (including identifying susceptibility) and treatment of various disorders associated with cytokine (in)activation e.g. chronic inflammation (esp) where associated with proteoglycan breakdown, such as rheumatoid arthritis) cancer (esp. development of metastases) and infections (esp. those caused by Gram negative bacteria). ecrosis factor-induced (glyco)protein mol. TSG-6 and its /- for treatment and diagnosis of chronic inflammatory a e.g. rheumatoid arthritis, infections, sepsis and TH, Vilcek J, Wisniewski 3; 122pp; English (DYNY ) UNIV NEW YORK STATE 1992-284330/34. B. 027190. Claim 1; Fid conditions antibody N-PSDB Tumour cancer

Page 58-59; 76pp; English.

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Gaps

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Score 262; DB 18; Pred. No. 1.6e-19; 5; Mismatches 43;

16;

14.18;

277 AA;

112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155 

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; Gaps 52 DTIVGVFHLRSPLGOYKLIFDRAREACANEAAIMAIYNOLSYXOKAKYHLCSAGWLEIGR 111 ö Ouery Match 14.1%; Score 262; DB 13; Length 277; Best Local Similarity 43\3%; Pred. No. 1.6e-19; Matches 45; Conservative, 16; Mismatches 43; Indels 112 VAYPTAFASONCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155 ò

TSG-6; human; tumour necrosis factor-stymulated gene-6 protein; treat; inflammatory disease; cancer-related pathology; inhibit; metastasis; invasive tumour growth; rhematoid arthritis; cachexia; atherosclerosis; systemic lupus erythematosus; rational dryg design. Tumour necrosis factor-stimulated gend-6 protein. W13654 standard; protein; 277 AA WO9704075-A1 07-NOV-1997 W13654; Ношо 

ilagnosis; cytokine; immune disorder; autoinmune disorder; infection; inflammatory disease; neurodegenerative disease; cancer; hepatitis.

'note= "putative signal sequence"

Location/Qualifiers

Pept1de

Tumour necrosis factor stimulated gene 6 (TSG-6) protein.

W84087 standard; Protein; 277 AA.

fumour necrosis factor stimulated gene 6; TSG-6;

File Copy 118..120 7.00te "potential Asn-glycosylation site" 258..260 7.00te "potential Asn-glycosylation site" "mature protein' Vilcek J, Wisniewski 94US-0242097. 91US-0642312. 93US-0024868. 94US-0242097 (UYNY ) UNIV NEW YORK STATE /note= 118..12 Modified-site Modified-site 13-MAY-1994; 14-JAN-1991; 01-MAR-1993; US5846763-A 08-DEC-1998 Lee TH, Protein 

Vilcek J, Wisniewski H;

WPI; 1997\*132619/12. Cronstein BN,

(UYNY ) UNIV NEW YORK STATE

20-JUL-1995;

06-FEB-1997

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This represents a human tumour necrosis factor stimulated gene 6 (TSG-6) protein. A prokaryotic host cell transformed, or a eukaryotic host cell transfected with expression vectors containing the TSG-6 nucleic acid are used to produce recombinant human TSG-6 protein. TSG proteins, peptide fragments of TSG proteins or antibodies to TSG proteins are useful for diagnosis or therapy of diseases mediated by cytokine activity or inactivity, such as immune and autolimmune disorders, infections, inflammatory diseases, neurodegenerative diseases, cancer and alcohol-
                                                                     DNA encoding tumour necrosis factor stimulated gene 6 protein -
useful for producing recombinant protein for diagnosis and therapy
of disease e.g. immune disorders or cancer
                                                                                                                                                                   Claim 2; Fig 3A-C; 65pp; English
WPI; 1999-059056/05
N-PSDB; V71778.
                                                                                                                                                                                                                                                                                                                                                                                                           induced hepatitis.
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Gaps ô 14.1%; Score 262; DB 20; Length 277; 43.3%; Pred. No. 1.6e-19; Live 16; Mismatches 43; Indels Conservative Ouery Match Best Local Similarity Matches 45; Conserv

277 AA;

Sequence

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DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111 : ||:| : |:|||: :|-||| | :|||||| :| :|-||||: || 32 eraagvyhrearsgkykltyaeakavcefegghlatykqleaarkigfhvcaagwmakgr 91 22

> a ä 셤

112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155

13381 standard; Protein; 360 AA.

Amino adid sequence of protein PRO271.

(first entry)

25-JUN-1999

Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Elison syndrome; gastrointestinal ulceration; congenital macrovilus atrophy; skin disease; cell growth; abnormal kerathocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; Als; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; vound healing; tissue repair.

Homo sapiens.

W09914328-A2

25-MAR-1999

98WO-US193 16-SEP-1998; 17-SEP-1997 17-SEP-1997 17-SEP-1997 17-SEP-1997 

970S-0059115. 970S-0059117. 970S-0059119. 970S-0059121. 97US-0059122. 97US-0059184. 97US-0059263. 97US-0066840 97US-0059113 97US-0059266 97US-0062125 97US-0062285 17-SEP-1997; 17-SEP-1997; 18-SEP-1997; 15-OCT-1997; 17-OCT-1997; 17-SEP-1997 18-SEP-1997

97US-0063120. 97US-0063120. 97US-0063121. 970S-0064248. 970S-0065186. 970S-0065186. 970S-0065846. 970S-0065693. 97US-0063435. 97US-0063435. 97US-0063704. 97US-0066772\ 97US-0066466 97US-0063550 97US-0066770 97US-0063128 97US-0066453 97US-0063127 97US-0063541 970S-0066364 97US-0( 24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 34-0CT-1997; 24-0CT-1997; 28-0ck-1997 28-0cf 1997 28-OCT-1997 29-0CT-1997 31-OCT-1997 12-NOV-1997 28-OCT-1997 39-OCT-1997 29-OCT-1997 29-0CT-1997 29-OCT-1997 29-OCT-1997 31-OCT-1997 03-NOV-1997 07-NOV-1997 17-NOV-1997 18-NOV-1997 -NOV-1997 24 - NOV - 1997 28-OCT-1997 29-OCT-1997 21-NOV-1997 24-NOV-1997 

Yuan J; Wood WI, Ď, Pennica Gurney AL, Chen J, Goddard A,

(GETH ) GENENTECH INC.

N-PSDB; X52252

WPI; 1999-229533/19.

used in, e.g. treatment of New isolated human genes and polypeptides gastrointestinal ulceration

Claim 12; Fig 78; 320pp; English.

The CDNA sequences are obtained from cDNA librahies, prepared from fetal lung, fetal lung, fetal librahies, prepared from fetal lung, fetal menched promoted for fetal kidney, fetal brain, fetal lung, fetal menched promoted for lung, fetal states have specific uses based on their homology to recorded polypeptides, e.g. PR0211 and PR0217 can be used for disorders associated with the preservation and maintenance of pastrointestinal mucosa and the repair of acute and chronic mucosal legions.

(e.g. enterocolitis, zollinger-Ellison syndrome, gastraintestinal mucosa and congenital microvillus artophy), skin disease associated with abnormal keratinocyte differentiation (e.g. psorias)s, epithelial cancers such as lung squamous cell carcinoma of the vulva and gilomas), concert effects on cell growth and development, disease, Akaheimer's profit entering protomating proceed as a target for anti-tumor drugs. PR0255 can be used as an atarget for anti-tumor drugs. PR0253 may be used in the trantment of Usher Syndrome or Atrophia areata; PR0269 can be used as an atarget for anti-tumor drugs. PR0269 can be used as an anti-tumor drugs. PR0269 can be used as an enterpeutic applications in wound healing and dissue repair; PR0319 can be used for treating problems of the kidney, uterus, endometrium, blood very

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# F. La Co My SEQ 1D 11, Database; SPTREMBL-15 us-09-466-778-11. Irspt Ac. NO. 99NRY3, 99UF98 Page, 1

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

April 4, 2001, 13:04:01; Search time 27.49 Seconds (without alignments) 1505.071 Million cell updates/sec Run on:

US-09-466-778-11 1857 1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

374700 seqs, 117207915 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_15:\*
1: Sp\_archea:\*
2: sp\_hacteria:\*
3: sp\_fung1:\*
4: sp\_human:\*
5: sp\_invertebrate:\* sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_organelle:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

					SUMMAKIES	
		æ				
Result No.	Score	Query Match	Query Yatch Length DB	DB	ID	Description
				1		
1	1757	94.6	897	4	Q9NRY3	Q9nry3 homo sapien
7	1468	79.1	1069	4	Q9UF98	Oguf98 homo sapien
٣	662	35.6	2212	4	093072	093072 homo sapien
4	645.5	34.8	2570	4	Q9NY15	Q9ny15 homo sapien
2	264	14.2	275	11	008859	O08859 mus musculu
9	177	9.5	2109	13	P79787	P79787 gallus gall
7	169.5	9.1	355	11	Q921X7	Q9z1x7 mus musculu
80	162	8.7	1321	4	014594	014594 homo sapien
თ	161.5	8.7	655	11	088564	088564 rattus norv
10	161.5	8.7	1290	13	Q9W6E1	Q9w6el gallus gall
11	160.5	8.6	2394	9	077610	077610 bos taurus
12	153	8.2	192	9	002817	002817 oryctolagus
13	153	8.3	929	9	077612	077612 bos taurús
14	151.5	8.5	1643	ø	077611	077611 bos taurus
15	151.5	8.2	3381	ø	017609	077609 bos taurus
16	126.5	9.9	103	9	Q9TTB3	Q9ttb3 sus scrofa
17	120.5		103	9	046380	046380 oryctolagus
18	110		396	13	Q9W6S4	Q9w6s4 gallus gall
19	109	5.9	302	4	Q9UNF4	Q9unf4 homo sapien

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	Q9y5y7 homo sapien Q93791 caenorhabdi		P87357 brachydanio	Q9ibg4 xenopus lae	070474 rattus norv	Q9ntm2 homo sapien	Q90656 gallus gall	057462 brachydanio	O60494 homo sapien	Q9qyx8 mus musculu	Q20204 caenorhabdi	Q9wuh9 rattus norv	Q92493 homo sapien	016004 lytechinus	008779 rattus norv	Q9v7f8 drosophila	Q9xyv4 drosophila	Q9v7f9 drosophila	070509 rattus norv	Q9uj36 homo sapien	097569 ceratother	Q91902 xenopus l		P79754 fugu rubrip	Q9sf50 arabidopsis	
	4 Q9Y5Y7 5 Q93791	5 023587	13 P87357	13 Q9IBG4	11 070474	4 Q9NTM2	13 Q90656	13 057462	4 060494	11 Q9QYX8	5 Q20204	11 о9wпн9	4 092493	5 016004	11 008779	5 Q9V7F8	5 Q9XYV4	5 Q9V7F9	11 070509	4 Q90J36	6 097569	13 Q91902	10 024530	13 P79754	10 Q9SF50	
	322 1584	3507	717	778	816	682	728	802	3623	780	1440	2906	294	2531	780	1480	1504	1504	364	742	364	721	261	1328	637	
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	109 105	104	103.5	102.5	100	99.5	99.5	99.2	99.5	66	66	66	86	86	97.5	97.5	97.5	97.5	96	96	95.5	95.5	95	94.5	94	
	20 21,	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

13 1 13	OGNRY3 PRELIMINARY; PRT; 897 AA. OGNRY3;	2000 (TrEMBLrel.	(TrEMBLrel. 15,	-	Chordata;	Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	NCBL_TaxID=9606;	[1]	SEQUENCE FROM N.A.	Tao Q., Zhang W., Cao X.;	"Molecular cloning and characterization of human FELL sharing homology	with CD44.";	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.	EMBL; AF160476; AAF82398.1;	SEQUENCE 897 AA; 97585 MW; EB920AF36101E388 CRC64;	Query Match 94.6%; Score 1757; DB 4; Length 897;	Za.	1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLODNGQCHADAKCVDLHFQDTTVGVFHL 60	489 MIGPGKHKCECKSHYVGDGLNCEPEQLFIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 548	61 RSPLGQYKLTFDKAREACANEAATWATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120	549 RSPLGQYKLTFDKAREACANEAATWATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFAS 608	121 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180	609 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFP 668	181 SLINFLIEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGLGENETLSGRDIEHHLAN 240	669 SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGTLEVPQNSGLGENETLSGRDIEHHLAN 728
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Conservative
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INTERPRO; IPR000561;
INTERPRO; IPR000782;
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                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                          SRXLKAPPAPVTLXHTXLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
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                                                                                               Indels
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALIJ3021; CAR61358.1; -
HASSP; P98066; 1TSG.
INTERPRO; IPR000538; -.
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Last sequence update)
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Pred, No. 1.2e-133;
4; Mismatches 29;
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01-OCT-2000 (TrEMBLrel. 15, Last annotation
HYPOTHETICAL 115.7 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
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80.5%;
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SEQUENCE 1069 AA;
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2036 NATLLSAN-ASOGKLEPAHSGLSLIISDAGPDNSSWAPVAPGTVVVSRIIVWDIMAFNGI 2094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97191544; PubMed-9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Panaka A., Kotaki H., Miyajima N., Momura N., Momura N., Perdiction of the coding sequences of unidentified human genes. VI. The coding sequences of Word of the coding sequences of unidentified human genes. VI. and coding sequences of the coding sequences of constant of the coding sequences of the coding sequences of the coding sequenced by analysis of constant coding constant of constant of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 NVSMFFYNDLVNGTILQTRLGSKLLITDR---QDPLHPTETRCVDGRDTLEWDICASNGI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 PSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFXPQNSGLGENETLSGRDIEHHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 THVISRXLKAPPAPVTLXHTXLGXGIFXXIILVTGAV--ALAAYSYFRINRKTIGF 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_Taxtp=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237451 MW; 4A954 $ 0504129134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFS
                                                                                                   01-FEB-1997 (TrEMBLrel. 02, Created)
0A-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01>CT-2000 (TrEMBLrel. 15, Last annotation update)
MYEDQBLAST KIAA0246 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.6%; Score 662; DB 4;
40.2%; Pred. No. 4.9e-55;
tive 47; Mismatches 158
2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01186; EGF_2; 13.
PROSITE; PS01241; LINK; UNKNOWN_1.
PROSITE; PS01248; LAMININ_TYPE_EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1265; LINKMODULE.
PROSITE; PSO0022; EGF_1; UNKNOWN_5
PROSITE; PSO0086; CYTOCHROME_P459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 3:321-329(\)996).
EMBL, D87433; BAA133\\7.1; -14SSP; P98066; ITSG.
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